

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 26, 2005, 01:06:48 ; Search time 519 Seconds  
(without alignments)  
680.784 Million cell updates/sec

Title: *the dm qw*  
US-10-666-642-194\_COPY\_111\_164

Perfect score: 298  
Sequence: 1 DGFMRKTKKSVQNKINR.....RVERGDGDAAYVITTEGVGH 54

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7331713 seqs, 327154945 residues

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10666642/runat\_25082005\_130057\_24954/app query.fasta\_1.199  
-DB=Published\_Applications\_NA -QFWT=fastap -SUFFIX=rpnp -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousem62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10666642@cgn2\_1.1.798 @runat\_25082005\_130057\_24954  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBBLCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2\_6/ptodata/1/pubnpa/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubnpa/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubnpa/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubnpa/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubnpa/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubnpa/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubnpa/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubnpa/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubnpa/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubnpa/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubnpa/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubnpa/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubnpa/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubnpa/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubnpa/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubnpa/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubnpa/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubnpa/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubnpa/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubnpa/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubnpa/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubnpa/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubnpa/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubnpa/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubnpa/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubnpa/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	100.0	585	18	US-10-412-699B-805
2	249	83.6	641	18	US-10-425-114-12391
3	249	83.6	823	18	US-10-412-699B-1614
4	249	83.6	880	19	US-10-767-701-11768
5	249	83.6	1039	20	US-10-425-115-73408
6	249	83.6	1663	17	US-10-374-780A-1531
7	249	83.6	1663	18	US-10-412-699B-1621
8	248	83.2	680	18	US-10-412-699B-1613
9	248	83.2	743	18	US-10-412-699B-1612
10	248	83.2	802	20	US-10-425-115-93169
11	247	82.9	666	19	US-10-437-963-63714
12	247	82.9	952	18	US-10-425-114-10354
13	247	82.9	974	18	US-10-424-599-115917
14	247	82.9	974	18	US-10-412-699B-1609
15	244	81.9	580	20	US-10-425-115-74300
16	244	81.9	1696	17	US-10-374-780A-1530
17	244	81.9	1696	18	US-10-412-699B-1620
18	243	81.5	669	19	US-10-767-701-1686
19	243	81.5	834	18	US-10-412-699B-1615
20	243	81.5	834	20	US-10-425-115-90976
21	242	81.2	352	20	US-10-856-499-1204
22	242	81.2	603	20	US-10-425-115-132529
23	242	81.2	821	19	US-10-437-963-77029
24	242	81.2	825	17	US-10-374-780A-1529
25	242	81.2	825	18	US-10-412-699B-1616
26	242	81.2	961	19	US-10-437-963-55249
27	242	81.2	999	20	US-10-425-115-170166
28	239	80.2	1235	18	US-10-424-599-112793
29	239	80.2	1235	18	US-10-412-699B-1608
30	237	79.5	1120	19	US-10-437-963-34431
31	232	77.9	999	17	US-10-374-780A-1532
32	232	77.9	999	18	US-10-412-699B-1622
33	232	77.9	1092	19	US-10-437-963-31295
34	230	77.2	748	10	US-09-533-029-29
35	230	77.2	748	10	US-09-534-455-195
36	230	77.2	748	17	US-10-225-066A-1
37	230	77.2	748	17	US-10-374-780A-253
38	230	77.2	748	18	US-10-412-699B-807
39	230	77.2	748	22	US-10-225-066A-1
40	202	67.8	577	18	US-10-424-599-115975
41	197	66.1	724	10	US-09-533-029-15
42	197	66.1	724	14	US-10-278-173-63
43	197	66.1	724	18	US-10-412-699B-85
44	197	66.1	1306	17	US-10-225-066A-1033
45	197	66.1	1306	17	US-10-374-780A-2611

RESULT 1

US-10-412-699B-805  
; Sequence 805, Application US/10412699B  
; Publication No. US20040045049A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Zhang, James  
; APPLICANT: Fromm, Michael E.  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Broun, Pierre E.  
; APPLICANT: Pineda, Omaira  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddie, James S.  
; APPLICANT: Yu, Guo-Liang

ALIGNMENTS

```
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 805
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1274
US-10-412-699B-805

Alignment Scores:
Pred. No.: 7,258-35 Length: 585
Score: 238.00 Matches: 54
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-412-699B-805 (1-585)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg 20
Db 331 GATGGTTTAAATGAGGAGGATGCGAAGAAATCTGTCAAAACCAACATTAAACAAGAGG 390

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db 391 AATTACTACAAATGCTCAAGTGAAGGTTGCTCGGTGAAGAGGAGGAGGAGAGAGTGT 450

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Db 451 GACGATGCAGCTTATGTAAATTACACATATGAGGATCCAT 492

RESULT 2
US-10-425-114-12391
; Sequence 12391, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12391
; LENGTH: 641
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 701174191_FLI
US-10-425-114-12391

Alignment Scores:
Pred. No.: 2,02e-27 Length: 641
Score: 249.00 Matches: 44
Percent Similarity: 88.89% Conservativeness: 4
Best Local Similarity: 81.48% Mismatches: 6
Query Match: 83.56% Indels: 0
DB: 18 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-10-425-114-12391 (1-641)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg 20
Db 106 GACGGATTCAAGTGGAGGAAGTACGGGAAGAAAGCCGCTCAAGAACAGCCCAATCCAAAGG 165

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db 166 AACTACTACCCGCTGCTGTCGAGGGGTCGCGGTGAAGAACGGGTGGAGGAGGACCGC 225

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Db 226 GACGACCCCGCTAGCTCATCACCACCTACGACGCGGTCCAC 267

RESULT 3
US-10-412-699B-1614
; Sequence 1614, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: DuBell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
```

US-10-374-780A-1531  
; Sequence 1531, Application US/10374780A  
; Publication No. US20040019927A1

GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddle, James E  
APPLICANT: Broun, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Dubell III, Arnold T  
APPLICANT: Pineda, Omaira  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374,780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1531  
LENGTH: 1663  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G1275  
US-10-374-780A-1531

Alignment Scores:  
Pred. No.: 7,35e-27 Length: 1663  
Score: 249.00 Matches: 44  
Percent Similarity: 88.89% Conservative: 4  
Best Local Similarity: 81.48% Mismatches: 6  
Query Match: 83.56% Indels: 0  
DB: 17 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x US-10-374-780A-1531 (1-1663)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
DB 1078 GACGGATTCAAGTGGAGGAAGTACCGGAAGAGCGGTCACGAACAGCCCAATCCAAAGG 1137  
QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40  
DB 1138 AACTACTACCGTCTGCTCGAGGGGCTGCGGCGTGAAGACGGGTGGAGAGGACCGC 1197  
QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
DB 1198 GACGACCCCGCTACGTATCATCCACCTACGACGGCGTCCAC 1239

RESULT 7

US-10-412-699B-1621

; Sequence 1621, Application US/10412699B

Publication No. US20040045049A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc J.  
APPLICANT: Broun, Pierre E.  
APPLICANT: Pineda, Omaira  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddle, James S.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Samaha, Raymond R.  
APPLICANT: Pilgrim, Marsha L.  
APPLICANT: Creelman, Robert A.  
APPLICANT: DuBell, Arnold N.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Kumimoto, Roderick  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MBI-0048CIP  
CURRENT APPLICATION NUMBER: US/10/412,699B  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/489,376  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 09/506,720  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,392  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,648  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/819,142  
PRIOR FILING DATE: 2001-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2011  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1621  
LENGTH: 1663  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-412-699B-1621  
Alignment Scores:  
Pred. No.: 7,35e-27 Length: 1663  
Score: 249.00 Matches: 44  
Percent Similarity: 88.89% Conservative: 4  
Best Local Similarity: 81.48% Mismatches: 6  
Query Match: 83.56% Indels: 0  
DB: 18 Gaps: 0  
US-10-666-642-194\_COPY\_111\_164 (1-54) x US-10-412-699B-1621 (1-1663)  
QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
DB 1078 GACGGATTCAAGTGGAGGAAGTACCGGAAGAGCGGTCACGAACAGCCCAATCCAAAGG 1137  
QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40  
DB 1138 AACTACTACCGTCTGCTCGAGGGGCTGCGGCGTGAAGACGGGTGGAGAGGACCGC 1197  
QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54





Db 376 GATGATACAAAGTGGAGAGTACGGCAAGAGTCCGTGAAGACAGTCCCAATCTAAGG 435  
Qy 21 AsnTyTrTyLysCysSerSerGluGlyCysSerVallyLysArgValGluArgAspGly 40  
Db 436 AACTACTACAAATGTTCAAGTGGAGGATGTCAGTGTGAAGAAAGGGTGGAAAGGGATAGA 495  
Qy 41 AspAspAlaAlaTyTrValIleThrThrTyTrGluGlyValHis 54  
Db 496 GATGACTACAGCTACGTGTATCAACATATGATGAAGGTGTGCAC 537  
RESULT 13  
US-10-424-599-115917  
; Sequence 115917, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 115917  
; LENGTH: 974  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75684C.1  
US-10-424-599-115917  
Alignment Scores:  
Pred. No.: 7,13e-27 Length: 974  
Score: 247.00 Matches: 45  
Percent Similarity: 90.74% Conservative: 4  
Best Local Similarity: 83.33% Mismatches: 5  
Query Match: 82.89% Indels: 0  
DB: 18 Gaps: 0  
US-10-666-642-194\_COPY\_111\_164 (1-54) x US-10-424-599-115917 (1-974)  
Qy 1 AspGlyPheLysTrpArgLysTyTrGlyLysSerVallyLysAsnAsnIleAsnLysArg 20  
Db 393 GATGATACAAAGTGGAGAGTACGGCAAGAGTCCGTGAAGAGCGTCCCAATCTAAGG 452  
Qy 21 AsnTyTrTyLysCysSerSerGluGlyCysSerVallyLysArgValGluArgAspGly 40  
Db 453 AACTACTACAAATGTTCAAGTGGAGGATGTCAGTGTGAAGAAAGGGTGGAAAGGGATAGA 512  
Qy 41 AspAspAlaAlaTyTrValIleThrThrTyTrGluGlyValHis 54  
Db 513 GATGACTACAGCTACGTGTATCAACATATGATGAAGGTGTGCAC 554  
RESULT 14  
US-10-412-699B-1609/c  
; Sequence 1609, Application US/10412699B  
; Publication No. US20040045049A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Zhang, Michael E.  
; APPLICANT: Fromm, Michael E.  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Broun, Pierre E.  
; APPLICANT: Pineda, Onaira  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddle, James S.  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Samaha, Raymond R.

; APPLICANT: Pilgrim, Marsha L.  
; APPLICANT: Creelman, Robert A.  
; APPLICANT: DuBell, Arnold N.  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Kumimoto, Roderick  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: MBI-0048CIP  
; CURRENT APPLICATION NUMBER: US/10/412,699B  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: 09/394,519  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: 09/489,376  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: 09/506,720  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: 09/533,030  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,392  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,029  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/532,591  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/533,648  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/713,994  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 09/819,142  
; PRIOR FILING DATE: 2001-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2011  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1609  
; LENGTH: 974  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-412-699B-1609  
Alignment Scores:  
Pred. No.: 7,13e-27 Length: 974  
Score: 247.00 Matches: 45  
Percent Similarity: 90.74% Conservative: 4  
Best Local Similarity: 83.33% Mismatches: 5  
Query Match: 82.89% Indels: 0  
DB: 18 Gaps: 0  
US-10-666-642-194\_COPY\_111\_164 (1-54) x US-10-412-699B-1609 (1-974)  
Qy 1 AspGlyPheLysTrpArgLysTyTrGlyLysSerVallyLysAsnAsnIleAsnLysArg 20  
Db 582 GATGATACAAAGTGGAGAGTACGGCAAGAGTCCGTGAAGAGCGTCCCAATCTAAGG 523  
Qy 21 AsnTyTrTyLysCysSerSerGluGlyCysSerVallyLysArgValGluArgAspGly 40  
Db 522 AACTACTACAAATGTTCAAGTGGAGGATGTCAGTGTGAAGAAAGGGTGGAAAGGGATAGA 463  
Qy 41 AspAspAlaAlaTyTrValIleThrThrTyTrGluGlyValHis 54  
Db 462 GATGACTACAGCTACGTGTATCAACATATGATGAAGGTGTGCAC 421  
RESULT 15  
US-10-425-115-74300  
; Sequence 74300, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B

```

; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 74300
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_167760C.1
US-10-425-115-74300

```

```

Alignment Scores:
Pred. No.:      1e-26      Length:      580
Score:          244.00     Matches:     43
Percent Similarity: 88.8%   Conservative: 5
Best Local Similarity: 79.63% Mismatches:    6
Query Match:      81.88%   Indels:      0
DB:               20      Gaps:        0

```

US-10-666-642-194\_COPY\_111\_164 (1-54) x US-10-425-115-74300 (1-580)

```

QY      1  AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
Db      389 GATGGATTCAATGGAGGAAGTATGCCAAGAGAGGCTGTCAAGAGTAGCCCAATCCAAGG 448

QY     21.  AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db     449 AACTACTACCGCTGCTGTCGGAGGGCTGCGCGGTGAAGAGCGGGTGGAGAGGCCGCC 508

QY     41  AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db     509 GAGACCCCGCGTACGTCAATCACCACCTACGACGGGCTCCAC 550

```

Search completed: August 26, 2005, 05:03:58  
Job time : 527 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 25, 2005, 23:29:33 ; Search time 140 Seconds  
(without alignments)

631.135 Million cell updates/sec

Title: US-10-666-642-194\_COPY\_111\_164

Perfect score: 298

Sequence: 1 DGFWRKRYGKSKVNNINKR.....RVERDGDAAAYVITTYBGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n\_model -DEV=xlh  
-Q=/cgn2\_1/USPRO\_pool/US10666642/runat 25082005 130054 24882/app query.fasta\_1.199  
-DB=Issued Patents NA -QFWT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10666642 cGcn 1.1 177 @runat 25082005 130054 24882 -NCPUS=6 -ICPU=3  
-NO MAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242	81.2	352	4	US-09-640-211A-1204
2	230	77.2	748	4	US-09-533-029-29
3	197	66.1	724	4	US-09-533-029-15
4	191	64.1	471	4	US-09-640-211A-1406
5	191	64.1	878	4	US-09-533-029-116
6	190	63.8	527	4	US-09-640-211A-1849
7	187	62.8	378	4	US-09-640-211A-1841
8	165	55.4	306	4	US-09-313-294A-4059
9	158	53.0	162	4	US-09-640-211A-1219
10	157.5	52.9	296	4	US-09-640-211A-1509
11	154.5	51.8	1130	4	US-09-533-029-27
12	153.5	51.5	561	4	US-09-640-211A-1580

13	151.5	50.8	1952	4	US-09-533-029-89	Sequence 89, Appl
14	145.5	48.8	319	4	US-09-640-211A-1487	Sequence 1487, Ap
15	145.5	48.8	1651	4	US-09-533-029-59	Sequence 59, Appl
16	145	48.7	385	4	US-09-640-211A-1531	Sequence 1531, Ap
17	137.5	46.1	351	4	US-09-640-211A-1694	Sequence 1694, Ap
18	137.5	46.1	488	4	US-09-640-211A-1504	Sequence 1504, Ap
19	130	43.6	337	4	US-09-640-211A-1309	Sequence 1309, Ap
20	129	43.3	340	4	US-09-640-211A-1498	Sequence 1498, Ap
21	127.5	42.8	1205	4	US-09-533-029-5	Sequence 5, Appl
22	123.5	41.4	360	4	US-09-640-211A-1358	Sequence 1358, Ap
23	120.5	40.4	557	4	US-09-640-211A-1435	Sequence 1435, Ap
24	117	39.3	520	4	US-09-640-211A-1238	Sequence 1238, Ap
25	116.5	39.1	1296	4	US-09-533-029-63	Sequence 63, Appl
26	112.5	37.8	425	4	US-09-640-211A-1424	Sequence 1424, Ap
27	104	34.9	567	4	US-09-640-211A-1269	Sequence 1269, Ap
28	103.5	34.7	1099	4	US-09-533-029-1	Sequence 1, Appl
29	88.5	29.7	2352	4	US-09-533-029-117	Sequence 117, App
30	75	25.2	351	4	US-09-640-211A-1248	Sequence 1248, Ap
31	65	21.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
32	65	21.8	1664976	4	US-09-692-570-1	Sequence 16724, A
33	64	21.5	138693	4	US-09-949-016-16724	Sequence 16928, A
34	64	21.5	524032	4	US-09-949-016-16928	Sequence 16929, A
35	64	21.5	524032	4	US-09-949-016-16929	Sequence 16930, A
36	64	21.5	524032	4	US-09-949-016-16930	Sequence 16931, A
37	64	21.5	524032	4	US-09-949-016-16931	Sequence 16932, A
38	64	21.5	529885	4	US-09-949-016-14340	Sequence 14340, A
39	64	21.5	529885	4	US-09-949-016-14341	Sequence 14341, A
40	64	21.5	529885	4	US-09-949-016-14342	Sequence 14342, A
41	64	21.5	529885	4	US-09-949-016-14343	Sequence 14343, A
42	64	21.5	529885	4	US-09-949-016-14344	Sequence 14344, A
43	64	21.5	529885	4	US-09-949-016-14345	Sequence 14345, A
44	64	21.5	529885	4	US-09-949-016-14346	Sequence 14346, A
45	64	21.5	529885	4	US-09-949-016-14347	Sequence 14347, A

ALIGNMENTS

RESULT 1  
US-09-640-211A-1204  
; Sequence 1204, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000.1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1204  
; LENGTH: 352  
; TYPE: DNA  
; ORGANISM: Eucalyptus grandis  
US-09-640-211A-1204

Alignment Scores: 6.51e-28 Length: 352  
Pred. No.: 242.00 Matches: 43  
Score: 85.19% Conservative: 3  
Percent Similarity: 79.63% Mismatches: 8  
Best Local Similarity: 81.21% Indels: 0  
Query Match: 4 Gaps: 0  
DB:

US-10-666-642-194\_COPY\_111\_164 (1-54) x US-09-640-211A-1204 (1-352)

Qy 1 AspGlyPheLysTpaGtGlytTyrGlyLysSerVallysAsnAsnIleAsnLysArg 20  
Db 184 GACGGATTCAAGTGGAGGAGTACCGGAGAGAGATGTTGTGAGACACTCCGATCCGAGG 243

Qy	21	Aen	Ty	Tyr	Lys	Cys	Ser	Ser	Clu	Gly	Cys	Ser	Val	Lys	Asp	Gly	40
Db	244	AAC	TACT	AT	TCGG	TGTT	TCGG	TGAA	GGCT	GTCT	CTGT	GAA	GAA	GAG	AGT	CGG	303
Qy	41	Asp	Asp	Ala	Ala	Tyr	Val	Ile	Thr	Thr	Tyr	Glu	Gly	Val	His	54	
Db	304	GAC	GAC	CCC	AA	GGT	TAT	GTA	TAA	TAA	CA	CAT	CAG	GGG	CA	345	

## RESULT 2

US-09-533-029-29  
; Sequence 29, Application US/09533029  
; Patent No. 666446  
; GENERAL INFORMATION:

```

, APPLICANT: Heard, Jacqueline
, APPLICANT: Broun, Pierre
, APPLICANT: Riechmann, Jose-Luis
, APPLICANT: Keddie, James
, APPLICANT: Pineda, Omaisra
, APPLICANT: Adam, Luc
, APPLICANT: Samaha, Raymond
, APPLICANT: Zhang, James
, APPLICANT: Yu, Guo-Liang
, APPLICANT: Ratcliffe, Oliver
, APPLICANT: Pilgrim, Marsha
, APPLICANT: Jiang, Cai-Zhong
, APPLICANT: Reuber, Lynne
, TITLE OF INVENTION: DISEASE-INDUCED
, FILE REFERENCE: MBI-010
, CURRENT APPLICATION NUMBER: US/
, CURRENT FILING DATE: 2000-03-22
, EARLIER APPLICATION NUMBER: 60/
, EARLIER FILING DATE: 1999-03-23
, NUMBER OF SEQ ID NOS: 121
, SOFTWARE: Patent In Ver. 2.1

```

Alignment Scores:	
Pred. No.:	1,286-25
Score:	230.00
Percent Similarity:	85.19%
Best Local Similarity:	75.93%
Query Match:	77.18%
DR:	4
Length:	748
Matches:	41
Conservative:	5
Mismatches:	8
Indels:	0
Gaps:	0

US-10-666-642-194 COPY 111 164 (1-54) x US-09-533-029-29 (1-748)

[illegible]

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 457 AACTACTACAAATGTTCAAGTGTGCTGCCCGTGAAGAAAGGGTGAACGACAGAGA 516

**Qy**            41 AspAspAlaalaTyrValIleThrThrTyrGluGlyValHis 54  
               |||||        ::::: ||||| ||||| ||||| |||||  
**Dh**            517 GATGATCCGAGCTTTGTGATAACAATTACGAGGGTCCCAC 55

### RESULT 3

US-09-533-029-15  
; Sequence 15, Application US/095333029  
; Patent No. 6664446  
; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline  
 ; APPLICANT: Broun, Pierre  
 ; APPLICANT: Riechmann, Jose-Luis  
 ; APPLICANT: Keddie, James

```

; APPLICANT: Pineda, Omaira .
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 724
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G179
; US-09-533-029-15

Alignment Scores:
Pred. No.: 1,34e-20 Length: 724
Score: 197.00 Matches: 33
Percent Similarity: 79.63% Conservative: 10
Best Local Similarity: 61.11% Mismatches: 11
Query Match: 66.11% Indels: 0
DB: 4 Gaps: 0

```

US-10-666-642-194 COPY 111 164 (1-54) X US-09-533-029-15 (1-724)

**Qy**      1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
          ||||| :  
**Db**      263 GATGGATCAGGTGGAGGAAGTAGCGCCAAAAAGCAGTCAAGAACAATTCATTCCCACGG 322

**Qy**      21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
          :::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
**D6**      323 AGTATTATTAAGTCACAGAAGAAGGATCGACTGAAGAAGCAAGTGCAAGGCCAATGG 382

QY      41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
         ||||| :|||::|||||:|||||:  
DQ    383 GGAGACGAAGCGAGCTGTGGTCACCATACCAGGCTGCAT 42

## RESULT 4

US-09-640-211A-1406  
; Sequence 1406, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:

APPLICANT: Wood, Marion  
APPLICANT: Shenk, Michael A  
APPLICANT: McGrath, Annette  
APPLICANT: Glenn, Matthew

Alignment Scores:		
Pred. No.:	6.05e-20	Length: 471
Score:	191.00	Matches: 33
Percent Similarity:	77.78%	Conservative: 9

```

Best Local Similarity: 61.11% Mismatches: 12
Query Match: 64.09% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1406 (1-471)

Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
Db 233 GATGGCTACAATGAGGAAGTACGGCCAGAAAGTGGTCAAGAACAGAGCTCCACCCAG 292

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40
Db 293 AGTATTACCGTTCGCTACAGTAAATTCGCGAGTGAAGAGAGGTCGACGGTGTGCG 352

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 353 GAAGATTGCGATGTTGATTAACGACCTACGAGGGCGACAT 394

RESULT 5
US-09-533-029-116
; Sequence 116, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; EARLIER FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 116
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1274
US-09-533-029-116

Alignment Scores:
Pred. No.: 1,45e-19 Length: 878
Score: 191.00 Matches: 35
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.09% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-116 (1-878)

Qy 20 ArgAsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAsp 39
Db 687 AGGATTACTACAATGCTCAAGTGAAGTTGCTCGGTGAAGAGAGGTTAGAGAGAT 746

Qy 40 GlyAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 747 GGTGACGATGCGAGCTTATGTAATTAACATATGAAGAGTCCAT 791

RESULT 6
US-09-640-211A-1849
; Sequence 1849, Application US/09640211A

```

```

; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1849
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1849

Alignment Scores:
Pred. No.: 1,01e-19 Length: 527
Score: 190.00 Matches: 33
Percent Similarity: 79.63% Conservative: 10
Best Local Similarity: 61.11% Mismatches: 11
Query Match: 63.76% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1849 (1-527)

Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20
Db 214 GATGGCTATAGATGGCGCAATATATGGCCAAAGGCTGTCAAAACACAGCCCTTTCCCGAGG 273

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40
Db 274 AGTATTACTGTTGTCACAAATGGAATGTCAGTGAAGAGAGAGTGGAGCGTTCGTCA 333

Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 334 GAAGATCCAGGAATTTGTATTAGCATATGAAGGACAGCAT 375

RESULT 7
US-09-640-211A-1841
; Sequence 1841, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1841
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1841

Alignment Scores:
Pred. No.: 1,81e-19 Length: 378
Score: 187.00 Matches: 33
Percent Similarity: 74.07% Conservative: 7
Best Local Similarity: 61.11% Mismatches: 14
Query Match: 62.75% Indels: 0
DB: 4 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1841 (1-378)

```



```
US-09-533-029-27
; Sequence 27, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaisra
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MEI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; FEATURE:
; OTHER INFORMATION: G291
; OTHER INFORMATION: "n" bases at various positions throughout the
; OTHER INFORMATION: sequence may be A, T, C, G, other or unknown
US-09-533-029-27

Alignment Scores:
Pred. No.: 7,77e-14 Length: 1130
Score: 154.50 Matches: 26
Percent Similarity: 74.55% Conservative: 15
Best Local Similarity: 47.27% Mismatches: 13
Query Match: 51.85% Indels: 1
DB: Gaps: 4

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-27 (1-1130)
Qy 1 AspGlyPheLysTrpAtqLysTyrGlyLysSerValLysAsnAenLleAenLysArg 20
Db 554 GATGGGTATCAATGAGGAAATATGGACAGAAAGTGACTAGAGACAATCCATCTCCCAAGA 613
Qy 21 AenTyrTyLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
Db 614 GCTTACTTCAATGTGCTGCTCCAGCTGTCTGTCACAAAGAGAGTTTCAGAGAGT 673
Qy 40 GlyAspAlaAlaTyrValLleThrTyrGluGlyValHis 54
Db 674 GTGAGGATCATGCTCGTGTAGTTCACATTTATGAGGGTGAACAC 718

RESULT 12
US-09-640-211A-1580
; Sequence 1580, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368

US-09-533-029-89
; Sequence 89, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaisra
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MEI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; FEATURE:
; OTHER INFORMATION: G186
; OTHER INFORMATION: "n" bases at various positions throughout the
; OTHER INFORMATION: sequence may be A, T, C, G, other or unknown
US-09-533-029-89

Alignment Scores:
Pred. No.: 4.8e-13 Length: 1952
Score: 151.50 Matches: 28
Percent Similarity: 70.91% Conservative: 11
Best Local Similarity: 50.91% Mismatches: 15
Query Match: 50.84% Indels: 1
DB: Gaps: 4

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1580 (1-561)
Qy 1 AspGlyPheLysTrpAtqLysTyrGlyLysSerValLysAsnAenLleAenLysArg 20
Db 272 GATGAATTCATGGCGGAAATATGGACAGAGCCCATTAAGGGCTCTCCACATCCCAAGA 331
Qy 21 AenTyrTyLysCysSer---GluGlyCysSerValLysLysArgValGluArgAsp 39
Db 332 GGTATTACAAATGCAGCAGCATGAGAGGTTCCTCTCAAGAAAGCAGTAGACGGGCC 391
Qy 40 GlyAspAlaAlaTyrValLleThrTyrGluGlyValHis 54
Db 392 CTGAGCATCAAAACGTATTGATTGTAACATATGAGGGCGGAACAC 436

RESULT 13
US-09-533-029-89
; Sequence 89, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaisra
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MEI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; FEATURE:
; OTHER INFORMATION: G186
; OTHER INFORMATION: "n" bases at various positions throughout the
; OTHER INFORMATION: sequence may be A, T, C, G, other or unknown
US-09-533-029-89

Alignment Scores:
Pred. No.: 4.8e-13 Length: 1952
Score: 151.50 Matches: 28
Percent Similarity: 70.91% Conservative: 11
Best Local Similarity: 50.91% Mismatches: 15
Query Match: 50.84% Indels: 1
DB: Gaps: 4
```

```
US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-89 (1-1952)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
Db 1036 GATGGATGTCAATGGAGAAAATATGCGCAGAAAGATGGCCAAAGGAATCCTTGTCCGCGG 1095
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
Db 1096 GCATATTACCGCTGACAGTGGCCAGCGGCTGTCGGTTCGCAACAAGTTCAAGTTGC 1155
QY 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Db 1156 GCGGAAGACAGATCAATCTGTATTACACCTACGAGGGAACCAT 1200

RESULT 14
US-09-640-211A-1487
; Sequence 1487, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1487
; LENGTH: 319
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1487

Alignment Scores:
Pred. No.: 3,12e-13 Length: 319
Score: 145.50 Matches: 25
Percent Similarity: 69.09% Conservative: 13
Best Local Similarity: 45.45% Mismatches: 16
Query Match: 48.83% Indels: 1
DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-640-211A-1487 (1-319)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
Db 146 GATGGACACCACTGGAGGAAGTATGGCAAAAAGATCACCAGGGACACCCCTTGTCCCGA 205
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
Db 206 GCTTACTTCAATGGCGCTCACGCTCCAGCTCCCTTGTCAAGAGAGGTGCAAAAGAGT 265
QY 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Db 266 GCTGAAGACCATCGTCACTATGCGACTTATGAAGCGGACAC 310

RESULT 15
US-09-533-029-59
; Sequence 59, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddle, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
```

```
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 59
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: GI417
US-09-533-029-59

Alignment Scores:
Pred. No.: 3,13e-12 Length: 1651
Score: 145.50 Matches: 27
Percent Similarity: 67.27% Conservative: 10
Best Local Similarity: 49.09% Mismatches: 17
Query Match: 48.83% Indels: 1
DB: 4 Gaps: 1

US-10-666-642-194_COPY_111_164 (1-54) x US-09-533-029-59 (1-1651)
QY 1 AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20
Db 749 GACGGATGTCAATGGAGAAAATACGGTCAGAAAATGGCGAAAGGGAATCCATGTCTCTGC 808
QY 21 AsnTyrTyrLysCysSer---SerGluGlyCysSerValLysLysArgValGluArgAsp 39
Db 809 GCTTATTATCGTTGCACCATGGCGGTGGATGTCTGTCCGTAAACAGGTCCAACGATGC 868
QY 40 GlyAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Db 869 GCGGAGGATACAATCTATCTTGACAAACACGTACCGAAGGAACCAT 913

Search completed: August 26, 2005, 01:48:30
Job time : 149 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 25, 2005, 19:45:28 ; Search time 2856 Seconds

(without alignments)  
916.170 Million cell updates/sec

Title: US-10-666-642-194\_COPY\_111\_164

Perfect score: 298

Sequence: 1 DGFWRKYGKSKVKNINR.....RVERDGDAAAYVITYGVGH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n\_model -DEV=xlh  
-Q=/cgn2.1/USPTO\_spool/US10666642/runat\_25082005\_130053\_24856/app\_query\_faeta\_1.199  
-DB=genEmbl -QWMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPFCU=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10666642 @CGN 1.1 4200 @runat\_25082005\_130053\_24856 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ats.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298	100.0	585	8	AF426252 Arabidops
2	242	81.2	707	8	AK109578 Oryza sat
3	242	81.2	792	8	AK066252 Oryza sat
4	242	81.2	839	8	AY341854 Oryza sat

c	5	242	81.2	149699	8	AP002486	Oryza sat
	6	237	79.5	1193	8	AK108555	Oryza sat
	7	232	77.9	983	8	AY341846	Oryza sat
	8	232	77.9	1091	8	AK108522	Oryza sat
	9	230	77.2	522	8	AY071847	Arabidops
	10	230	77.2	748	6	AR439815	Sequence
	11	197	66.1	444	8	AF426251	Arabidops
	12	197	66.1	548	8	AY085246	Arabidops
	13	197	66.1	696	8	AK118457	Arabidops
	14	197	66.1	724	6	AR439808	Sequence
	15	197	66.1	1200	8	AF442397	Arabidops
	16	197	66.1	1231	8	AY091224	Arabidops
	17	197	66.1	1809	8	AY063870	Arabidops
	18	196	65.8	147704	8	AC097112	Oryza sat
	19	195	65.4	1182	6	AX506986	Sequence
	20	195	65.4	1182	6	AX652016	Sequence
	21	195	65.4	1182	8	BT008482	Arabidops
	22	195	65.4	1182	8	AF418309	Arabidops
	23	195	65.4	1213	8	BT002338	Arabidops
	24	195	65.4	1264	8	AY114650	Arabidops
	25	195	65.4	1453	8	AY062720	Arabidops
	26	195	65.4	1462	8	AY045813	Arabidops
	27	195	65.4	1606	8	AY136318	Arabidops
	28	195	65.4	1667	8	CUSLDB	L44134 Cucumis sat
	29	194.5	65.3	129402	8	AP003341	Oryza sat
	30	194.5	65.3	158084	8	AP003492	Oryza sat
	31	194	65.1	864	8	AY071849	Arabidops
	32	194	65.1	1046	8	AK069091	Oryza sat
	33	194	65.1	1070	8	AY341858	Oryza sat
	34	194	65.1	1276	8	AY341859	Oryza sat
	35	193	64.8	1260	6	AX653470	Sequence
	36	193	64.8	1847	8	AF459793	Oryza sat
	37	193	64.8	1993	8	IPBSPFLP	D30038 Ipomoea bat
	38	193	64.8	2191	8	AK103745	Oryza sat
	39	193	64.8	2764	8	AK065078	Oryza sat
	40	192	64.4	1287	8	AK062027	Oryza sat
	41	192	64.4	1953	6	AX654708	Sequence
	42	192	64.4	2353	8	AK065518	Oryza sat
	43	192	64.4	2373	8	AB026890	Nicotiana
	44	192	64.4	2389	8	AB063576	Nicotiana
	45	191	64.1	657	8	AF404857	Arabidops

#### ALIGNMENTS

RESULT 1	AF426252	Arabidopsis thaliana WRKY transcription factor 51 (WRKY51) mRNA,	585 bp	mRNA	linear	PLN 08-NOV-2001
LOCUS	AF426252	Arabidopsis thaliana WRKY transcription factor 51 (WRKY51) mRNA,	585 bp	mRNA	linear	PLN 08-NOV-2001
DEFINITION	AF426252	complete cds.				
ACCESSION	AF426252	GI:16798361				
VERSION	AF426252.1	GI:16798361				
KEYWORDS	Arabidopsis thaliana (thale cress)					
SOURCE	Arabidopsis thaliana					
ORGANISM	Arabidopsis thaliana					
REFERENCE	1 (bases 1 to 585)					
AUTHORS	Kushnir, S., Ulker, B. and Somssich, I.E.					
TITLE	Direct Submission					
JOURNAL	Submitted (02-OCT-2001) Biochemistry, Max-Planck-Institut fur Zuchtungsforshung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829, Germany					
FEATURES	Location/Qualifiers					
source	1..585					
/organism="Arabidopsis thaliana"						
/mol_type="mRNA"						
/db_xref="taxon:3702"						
/chromosome="v"						
/clone="BAC MKK3"						
/tissue_type="inflorescence"						
/ecotype="Columbia"						

```

gene      1. .585
          /gene="WRKY51"
CDS       1. .585
          /gene="WRKY51"
          /codon_start=1
          /product="WRKY transcription factor 51"
          /protein_id="AA129429.1"
          /db_xref="GI:16798362"
          /translation="WNISQNPNTYSDENFINPWNDDNSLMPFDIDEGNNG
LIEEISPTSVISSETFGSGSGSATILSKESYTRNGSKESQTKETGHRVAFRI
RSKIDVMDGDFWRIYKGRKVNKNINKNYKCSGCVSKRVERDGDAAAYVITTY
EGVHNHESLSNYYNEMVLSYDHDNQHSLRS"

ORIGIN
Alignment Scores:
Pred. No.: 1,07e-30 Length: 585
Score: 298.00 Matches: 54
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AF426252 (1-585)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAAsnIleAsnLysArg 20
Db 331 GATGGTTTAAATCGAGGAAGTATGCGAAGAATCTGTCAAAACACATTAACGAGG 390

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Db 391 AATTACTACAAATGCTCAAGTGAAGGTTCTCGTGAAGAGAGGCGTAGAGAGATGGT 450

QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54
Db 451 GACGATGCAGCTTATGTATTAATTAACATATGAAGGAGTCCAT 492

RESULT 2
LOCUS AK109578 707 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-135-F06, full
insert sequence.
ACCESSION AK109578
VERSION AK109578.1 GI:32994787
KEYWORDS FL1 CDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE
1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamura,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M., and Hayashizaki,Y.

japonica rice
Collection, mapping, and annotation of over 28,000 cDNA clones from
Science 301 (5631), 376-379 (2003)
JOURNAL 22752273
MEDLINE 12869764
PUBMED
REFERENCE 2 (bases 1 to 707)

```

## AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ishikawa, M., Itoh, M., Kagawa, I., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, J., Kawai, J., Kawamura, M., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

## Direct Submission

## TITLE

## JOURNAL

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamura, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

## FEATURES

## source

1. 707  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/db\_xref="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="002-135-F06"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,7e-23 Length: 707  
Score: 242.00 Matches: 41  
Percent Similarity: 88.89% Conservative: 7  
Best Local Similarity: 75.93% Mismatches: 6  
Query Match: 81.21% Indels: 0  
DB: 8 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x AK109578 (1-707)

Qy	1	AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnLeuAsnLysArg	20
Db	245	GACGGGTTCAAGTGGCGAAAGTACGGGAAGAGCGGTGAAGACGACCGCGAACC	304
Qy	21	AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysValGluArgAspGly	40
Db	305	AACTACTACCGGTGCTCGCGCGGGGTGCGGCGTCAAGAGCGGGTGGAGCGCGACGC	364
Qy	41	AspAspAlaAlaTyrValIleThrTyrGluGlyValHis	54
Db	365	GACGACCGCGCGTACGTCGTCAACACCTACGACGGCGTCCAC	406

[illegible]

1. The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otono, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., KIKEN: Kawaj, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Havaehizaki, Y.

**TITLE** Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice  
**JOURNAL** Science 301 (5631): 376-379 (2003)

22752273  
12863764

2 (bases 1 to 792)

MEDLINE  
PUBMED  
REFERENCES  
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,  
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,  
Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Inamura, K.,  
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,  
Kagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,  
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,  
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,  
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,  
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,  
Namiki, T., Narikawa, R., Niikata, J., Nishi, K., Nomura, K.,  
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,  
Oeato, N., Oca, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,  
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,  
Shingamura, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,  
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,  
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,  
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,  
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and  
Yoshimura, A.

**TITLE**  
Direct Submission  
**JOURNAL**  
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of  
Genomics

Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail: skikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007]

COMMENT  
This clone is one of the 28K full-length cDNA clones from japonica rice.  
URL : <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahaeishi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

```

FEATURES
source
1..792
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J013052M10"

```

ORIGIN	Alignment Scores:	
Pred. No.:	5,368-23	Length: 792
Score:	242.00	Matches: 42
Percent Similarity:	90.74%	Conservative: 7
Best Local Similarity:	77.78%	Mismatches: 5
Query Match:	81.21%	Indels: 0
DB:	8	Gaps: 0

US-10-666-642-194 COPY 111 164 (1-54) x AK066252 (1-792)

QY 1 AspGlyPheLysTrpArgIysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20

Db 344 GATGCTTCAAGTGAGGAAGTACGSCAAGAAGCTGTCAAGAACAGCCCAATCCAAGA 403

21 AsnTyrTyrIysCysSerSerGluGlyCysSerValLysLysValGluArgAspGly 40

Db  
404 AACTACTACCGGTCGACCGAGGGGTGCAACGTGAAGCCAGTGGAGAGACCGG 463

Qy	41	AspAspAlaAlaIyVallIeThrThrTyC	CluGlyValHis	54
		:::		
		:::		
Db	464	GAGGACCAACCGCTACGTCATCACCACCTACGACGGCGTCCAC		505

[illegible]

KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 839)  
Yao,Q., Peng,R. and Xiong,A.  
Isolation of rice WRKY protein through W-box bait vector by  
modified yeast one-hybrid system method  
Unpublished  
2 (bases 1 to 839)  
Yao,Q., Peng,R. and Xiong,A.  
Direct Submission  
Submitted (14-JUL-2003) Bio-tech Center, Shanghai Academy of  
Agricultural Science, Beldi Road 2901, Shanghai, Shanghai  
021-201106, China  
Location/Qualifiers  
1. 839  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/db\_xref="taxon:39947"  
67..726  
/note="transcription factor"  
/codon\_start=1  
/product="WRKY13"  
/protein\_id="AAQ20913.1"  
/db\_xref="GI:33519196"  
/translation="MAASLGLCHETSAYSPASNTSSSLCPPLMADHIVDGGGGG  
CSFGRFLEHGHSVSLPLPPPPQPVVAGGNDOYGVSSSSAAATTRIGERTSE  
VEVLDDGPKWRVYKKAQKSSPNRYRCSAGGVKKVERDGDPRYVYVYDGV  
HNHATPGCVGGGHLPIPTSAAPPVSPFAAAASPPFAHQAWGAPLHAAAHSSSE  
F"  
ORIGIN  
Alignment Scores:  
Pred. No.: 5,73e-23 Length: 839  
Score: 242.00 Matches: 41  
Percent Similarity: 88.89% Conservative: 7  
Best Local Similarity: 75.93% Mismatches: 6  
Query Match: 81.21% Indels: 0  
DB: 8 Gaps: 0  
US-10-666-642-194\_COPY\_111\_164 (1-54) x AY341854 (1-839)  
QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnLysArg 20  
Db 388 GACGGGTTCAAGTGGCGAAAGTACGGGAAGAGCGGTGACAGCAGCCGCGG 447  
QY 21 AntTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgSpGly 40  
Db 448 AACTACTACCGGTGCTCGCGCGGGTCCGCGGTCAAGAACGGGTGGAGCGCAGCGC 507  
QY 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
Db 508 GACGACCCCGCTACGTCTGACCACTACGAGCGGTCCAC 549  
RESULT 5  
AP002486/c  
LOCUS  
DEFINITION  
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,  
PAC clone: P0510F03.  
ACCESSION  
AP002486 BA000010  
VERSION  
AP002486.1 GI:8468048  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1  
Sasaki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,  
Katayose,Y., Wu,J., Nimura,Y., Cheng,Z., Nagamura,Y.,  
Antonio,B.A., Kanamori,H., Hosokawa,S., Masukawa,M., Arikawa,K.,  
Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arica,K.,  
Hamada,M., Harada,C., Hijishita,S., Honda,M., Ichikawa,Y.,  
Idonuma,A., Iijima,M., Ikeda,M., Ikeno,M., Ito,S., Ito,T., Ito,Y.,  
Ito,Y., Iwabuchi,A., Kamiya,K., Karasawa,W., Katagiri,S.,  
Kikuta,A., Kobayashi,N., Kono,I., Machita,K., Maehara,T.,  
Mizuno,H., Mizubayashi,T., Mukai,Y., Nagasaki,H., Nakashima,M.,  
Nakama,Y., Nakamichi,Y., Nakamura,M., Namiaki,N., Negishi,M.,  
Ohta,I., Ono,N., Saji,S., Sakai,K., Shibata,M., Shimokawa,T.,  
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Tsuji,K., Waki,K.,  
Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,  
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,  
Yano,M., Jiang,J. and Gojobori,T.  
The genome sequence and structure of rice chromosome 1  
Nature 420 (6913), 312-316 (2002)  
22337376  
PUBMED  
12447438  
2 (bases 1 to 149699)  
Sasaki,T., Matsumoto,T. and Yamamoto,K.  
Direct Submission  
Submitted (07-JUN-2000) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program; Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasakia@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
The orientation of the sequence is from SP6 to T7 of the PAC clone.  
Genes were predicted from the integrated results of the  
following:GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as  
SplicePredictor (October1998 version). The genomic sequence was  
searched against the non-redundant database NRP (PIR,SWISSPROT,  
GENPEPT, PDB) from MAFY DNABank and the cDNA sequence database at  
RGF. Protein similarities of the coding regions were searched  
against NRP with BLASTP2.0. ESTs represent the identified cDNA  
sequences using BLASTN2.0 with the corresponding DDBJ accession no.  
and RGP clone ID.  
This sequence of this clone has an overlap with P0695A04 clone at  
the 3' end. This clone ends at the position 22,228 of P0695A04.  
Detailed information on overlap and assembly quality together with  
annotation of this entry at  
http://rgp.dna.affrc.go.jp/GenomeSeq.html.  
Location/Qualifiers  
1. 149699  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="1"  
/clone="P0510F03"  
complement(2698..3138)  
/note="3' LTR"  
4157..5053  
/note="unnamed protein product; Similar to Oryza sativa  
gypsy-type retrotransposon RIRE2; orf3 (AB030283)"  
/protein\_id="BAB03349.1"  
/db\_xref="GI:9558413"  
/translation="MTEKESFEGQWAPSDVTEENLKMVHAGVLPAKEIIGWRPACG  
EAFPTDTHVEVVFHFYFGFALTCKFFGILNFYGISLHLNINSIVHIANFVHV  
CEAFILRHPFALFRIFFLKPPQKNKPCVVGAGFQLRGTLTKSPFMTKNSKQ  
WHANWFQNPALPEYSCLPVYQDTWNSLPIGDEAAQALEMERLMLKEOGLQG  
EQITRHKELCLAPIKERSRTAFEDGKHDNRPDPSLDLPFKINKERMYKIFSNAIV  
SYSHQLPVVPVNAFNPPQVR1"  
5140..5922  
/note="unnamed protein product; Similar to Oryza sativa  
gypsy-type retrotransposon RIRE2; orf4 (AB030283)"  
/protein\_id="BAB03350.1"  
/db\_xref="GI:9558414"  
/translation="MKSDPPTQARRSPRQHTVQSGGPTIRSDPQOTSKPAQTGSR  
KKLVLDNDEDDDDNSKSGDKPTNPKPPKMPKRLAGQMPKIRTSRYKPLTILF  
RHASLIETIERNLTKPSDIDPTGKPDPAATEPNLSKDAKPTESQPTASSQPT  
AESQPTGAQSDKANPSDQPLTGNQSAATATTREPTTGNQSDVDLNOIPEAKAQ  
TTSQGPVGNDSVIGSPDKEQSPHAQPGTSSGNSSSQVMPF"  
6651..7112  
/note="unnamed protein product; Similar to Oryza sativa  
gypsy-type retrotransposon RIRE2; orf5 (AB030283)"  
/codon\_start=1



## AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team:  
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishihiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

2 (bases 1 to 1193)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyas, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice. URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.  
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyas, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

## FEATURES

source  
 1. .1193  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="002-144-E10"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.06e-22 Length: 1193  
 Score: 237.00 Matches: 40  
 Percent Similarity: 88.89% Conservative: 8  
 Best Local Similarity: 74.07% Mismatches: 6  
 Query Match: 79.53% Indels: 0  
 DB: 8 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x AK108555 (1-1193)

Qy 1 AspGlyPheLysTTPArgLysTyrGlyLysSerVallysAsnAsnLysArg 20

Db 515 GACGGGTATAGTGCAGGAGTACGGGAAAGTCCGTAAAGACAGCCCTAATCCGAGG 574

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerVallysLysArgValGluArgAspGly 40

Db 575 AACTACTACCGGTCTCGACGGAGGGGTGCAACGTGAAGAGAGAGGGTGGAGAGACAAAG 634

Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54

Db 635 AACGACCGCGGTACGGTGCAGTGTACGAGGGGATCCAC 676

RESULT 7

AY341846

LOCUS

AY341846

DEFINITION

Oryza sativa (japonica cultivar-group) WRKY5 mRNA, complete cds.

ACCESSION

AY341846.1 GI:33519179

VERSION

AY341846.1

KEYWORDS

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 983)

Yao, Q., Peng, R. and Xiong, A.

Isolation of rice WRKY protein through W-box bait vector by

modified yeast one-hybrid system method

Unpublished

2 (bases 1 to 983)

Yao, Q., Peng, R. and Xiong, A.

Direct Submission

Submitted (14-JUL-2003) Bio-Tech Center, Shanghai Academy of

Agricultural Science, Beidi Road 2901, Shanghai, Shanghai

021-201106, China

Location/Qualifiers

1. .983

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/db\_xref="taxon:39947"

40..780

/note="transcription factor"

/codon\_start=1

/product="WRKY5"

/protein\_id="AAQ20905.1"

/translation="MSSLYPSLILSLSESPEAYRQVGGRRVAGEDVDDDDMAAVADA

VSSLYLSDMDVVEYTFEVEGFHSKQHPFPVAAAPLAGGREGSRREAAVNLGKMDR

GPAPVSGAATGTVGFRSKNGSKIAFTKRSEVDVLDGGRWRKRYGKKWVKNSPNPNYY

CDS

```

RCSGCGRVKVRERDDARFVVTTVDGVNHPAPLHLRPLQPPPGGYSIAGAPAVV
APHGRGLGEAEVIALFRGTTATSLLLP"

ORIGIN
Alignment Scores:
Pred. No.: 1,53e-21 Length: 983
Score: 232.00 Matches: 40
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 74.07% Mismatches: 7
Query Match: 77.85% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AY341846 (1-983)

Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysAsnAsnLysArg 20
Dbb 451 GACGGCTACCGGTGGAGGAGTACGGCAAGAGTGGTCAAGAACAGCCCAACCCCAAGG 510
Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Dbb 511 AACTACTACCGGTGCTCGAGCGAGGGGTGCGCGTGAAGAGCGGGTGGAGCGCGCCGG 570
Qy 41 AspAlaAlaTyrValIleThrTyrGluGlyValHis 54
Dbb 571 GACGACGGCGCTCGTCTGCTCACCACCTACGACGCGCTCCAC 612

RESULT 8
AKI08522
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:002-144-B05, full
insert sequence.
ACCESSION
AKI08522
VERSION
AKI08522.1 GI:32993731
KEYWORDS
FLI cDNA; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otono,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Otsu,N., Oka,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M., and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL
MEDLINE
PUBMED
22752273
REFERENCE
2
(bases 1 to 1091)
AUTHORS
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiroaka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,

```

```

Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Otono,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S., and
Yoshimura,A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K., and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Oka,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A., and Hayashizaki,Y.
FEATURES
Location/Qualifiers
source
1..1091
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="002-144-B05"

ORIGIN
Alignment Scores:
Pred. No.: 1,73e-21 Length: 1091
Score: 232.00 Matches: 40
Percent Similarity: 87.04% Conservative: 7
Best Local Similarity: 74.07% Mismatches: 7
Query Match: 77.85% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AKI08522 (1-1091)

Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysAsnAsnLysArg 20
Dbb 455 GACGGCTACCGGTGGAGGAGTACGGCAAGAGTGGTCAAGAACAGCCCAACCCCAAGG 514
Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
Dbb 515 AACTACTACCGGTGCTCGAGCGAGGGGTGCGCGTGAAGAGCGGGTGGAGCGCGCCGG 574
Qy 41 AspAlaAlaTyrValIleThrTyrGluGlyValHis 54

```

```
|||||:::|||||:::|||||:::|||||:::|||||
Db 575 GACGAGCGCGCTGCTGCTACACCTAGCAGCGGCTCCAC 616

RESULT 9
AY071847
LOCUS
DEFINITION Arabidopsis thaliana WRKY transcription factor 50 (WRKY50) mRNA,
complete cds.
ACCESSION AY071847
VERSION AY071847.1 GI:18252116
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 522)
REFERENCE
AUTHORS Ulker,B., Kuhnir,S. and Somssich,I.E.
TITLE Arabidopsis thaliana transcription factor WRKY50
JOURNAL Unpublished
REFERENCE
AUTHORS Ulker,B., Kuhnir,S. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Biochemistry, Max-Planck-Institut fur
Zuchtungsforshung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
source
1..522
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="V"
/map="BAC clone T19G15"
/tissue_type="inflorescence"
/ecotype="Columbia"
1..522
/gene="WRKY50"
1..522
/gene="WRKY50"
/codon_start=1
/product="WRKY transcription factor 50"
/protein_id="AAL61857.1"
/db_xref="GI:18252117"
/translation="MNDADTNLGSFSDTHSVRFPELDLSDEWMDLLVSAGVGN
OSYGYQTSVAGALFSGSSCSFSPESHSTKYVAATATASADNQNKKEKKIKGRVA
FKTRSEVLDGCFWRKYGKKWKNSEFPRNYKCSVDGCPVKRVERDRDDPSFVI
TTYEGSHNHSNMN"

ORIGIN
Alignment Scores:
Pred. No.: 1,37e-21 Length: 522
Score: 230.00 Matches: 41
Percent Similarity: 85.19% Conservative: 5
Best Local Similarity: 75.93% Mismatches: 8
Query Match: 77.0% Indels: 0
DB: 8 Gaps: 0

US-10-666-642-194_COPY_111_164 (1-54) x AY071847 (1-522)
Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnLysArg 20
|||||:::|||||:::|||||:::|||||:::|||||
Db 340 GACGGGTTCAAGTGAGAGAAAGTATGGAGAGAGAGTGGTGAAGACAGCCACATCCAAGA 399

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40
|||||:::|||||:::|||||:::|||||:::|||||
Db 400 AACTACTACAAATGTTTCAGTTGCTGCTCCGCTGAAGAAAAGGTTGAACGACAGACA 459

Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54
|||||:::|||||:::|||||:::|||||:::|||||
Db 460 GATGATCCGAGCTTGTGTATACACTTACGAGGGTTCCAC 501

RESULT 10
AR439815
LOCUS
DEFINITION Arabidopsis thaliana WRKY transcription factor 45 (WRKY45) mRNA,
complete cds.
ACCESSION AF426251
VERSION AF426251.1 GI:16798359
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 444)
REFERENCE
AUTHORS Kuhnir,S., Ulker,B. and Somssich,I.E.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2001) Biochemistry, Max-Planck-Institut fur
Zuchtungsforshung, Carl-von-Linne-Weg 10, Koeln, NRW D-50829,
Germany
FEATURES
source
1..444
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="III"
/clones="BAC F28J7"
/tissue_type="inflorescence"
/ecotype="Columbia"
1..444
/gene="WRKY45"
```





HPFPMTPRGHIGMLTSPILDHGATTASSSFSPQPRYLLTQHHQPYNNYNNNSLSMI  
NRRSSDGTFTVNPFGPSSFPFGYDMSQASTSTSSIRDHGLLODILPQIRSDTINTQ  
TNEENKK"

ORIGIN

Alignment Scores:  
Pred. NO.: 1.01e-16 Length: 1200  
Score: 197.00 Matches: 33  
Percent Similarity: 81.48% Conservative: 11  
Best Local Similarity: 61.11% Mismatches: 10  
Query Match: 66.11% Indels: 0  
DB: 8 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x AF442397 (1-1200)

Qy	1	AspGlyPheLysTyrArgLysTyrGlyLysLysSerValLysAsnAsnLysArg	20
Db	664	GACGGTTATAGTGGAGGAAATACGGCCAAAGCTGTCAAAAACAGTCCTTATCCAGA	723
Qy	21	AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly	40
Db	724	AGCTATTACCGTTGCACCCACAGTGGGTTGCGAGTGAAGAGAGAGTGGAGATCCTCC	783
Qy	41	AspAspAlaIaIaTyrValIleThrThrTyrGluGlyValHis	54
Db	784	GATGATCCTTCGATCGTCATGACAACTACGAGGTCAGCAT	825

Search completed: August 26, 2005, 01:06:40  
Job time : 2881 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 25, 2005, 23:22:33 ; Search time 2304 Seconds  
(without alignments)  
892.131 Million cell updates/sec

Title: US-10-666-642-194\_COPY\_111\_164

Perfect score: 298

Sequence: 1 DGFKRWKYGKSKVRNNINKR.....RVERDGDAAAYVITYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/csm2\_1/USPTO\_epool/SUP1666642/runat\_25082005\_130054\_24868/app\_query.fasta\_1.199  
-DB=EST -QFMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10666642 @CGN 1.1 4352 @runat\_25082005\_130054\_24868 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_hic3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298	100.0	435	6	CD529340 02J01 Ara
2	253	84.9	643	6	CB879380 HP11P20T
3	253	84.9	700	1	AL503208 AL503208
4	253	84.9	849	2	BE412464 MCG004.A0
5	250	83.9	549	2	BF009428 ss78f04.Y
6	250	83.9	634	5	BU547499 GM880013A
7	250	83.9	671	4	BI209002 EST527042
8	249	83.6	412	5	BQ515840 EST623255
9	249	83.6	418	4	BI433746 EST536507

10	249	83.6	418	5	BQ515839	BQ515839	EST623254
11	249	83.6	466	6	CD967539	CD967539	SEW_126 G
12	249	83.6	497	2	AW744840	LGI_384 F	
13	249	83.6	504	2	BG049241	OVI_17 D0	
14	249	83.6	581	2	BE216050	HV_CEB000	
15	249	83.6	610	4	BM328984	PIC1_31 H	
16	249	83.6	690	2	AW565483	LGI_344 C	
c 17	249	83.6	722	5	BQ516647	EST624062	
c 18	249	83.6	736	4	BM334368	MEST136-B	
19	249	83.6	742	5	BQ516646	EST624061	
20	249	83.6	755	7	CN151030	WOUND1_73	
21	249	83.6	791	7	CN151116	WOUND1_73	
22	247	82.9	445	4	BI321739	saF98d06	
23	247	82.9	454	4	BI426331	saF09n11	
24	247	82.9	531	4	BI892650	saF36c06	
25	247	82.9	549	4	BM188076	saJ84d10	
26	247	82.9	596	5	BQ473633	saPl5g03	
27	247	82.9	666	9	CL971695	OB1FCC021	
28	245	82.2	375	5	BU578439	sa-53a02	
29	245	82.2	563	2	BE216105	HV_CEB000	
30	245	82.2	573	6	CB879922	HP11H01r	
31	244	81.9	599	4	BG525040	46-57 Ste	
32	244	81.9	673	5	BQ987474	QGF12F06	
33	244	81.9	710	5	BQ984602	QGE3d01.Y	
34	243	81.5	643	6	CF002660	QBH13h10	
35	243	81.5	649	6	CD233113	SSI_11_A0	
36	242	81.2	585	9	CL970459	OB1FCC019	
37	242	81.2	601	2	BE230596	99AS81 Ri	
38	241	80.9	566	6	CA156006	SCBPR2300	
39	240	80.5	727	7	CO817603	FA_SEA001	
40	239	80.2	559	5	BU577163	sa-56b10	
41	239	80.2	596	5	BQ742659	sa-54d08	
42	239	80.2	744	7	CO093096	GR_Ba14H	
c 43	239	80.2	745	7	CO093095	GR_Ba14H	
44	239	80.2	802	7	CK110138	N053D02 P	
45	239	80.2	819	7	CN140156	Ox1_34_A0	

ALIGNMENTS

CD529340 02J01 Arabidopsis Leaf Senescence Library Arabidopsis thaliana CDNA 3', mRNA sequence. EST 31-DEC-2003

CD529340

CD529340.1 GI:40449352

EST

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 435)

Guo,Y., Cai,Z. and Gan,S.

Transcriptome of Arabidopsis leaf senescence

Plant Cell Environ. 27 (5), 521-549 (2004)

Contact: Susheng Gan

Department of Horticulture

Cornell University

119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA

Tel: 607 254 5418

Fax: 607 255 0599

Email: sg288@cornell.edu

Insert Length: 435 Std Error: 0.00

Seq primer: T7

POLYA=No.

Location/Qualifiers

1. 435

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Landsberg erecta"

/db\_xref="taxon:3702"

FEATURES

source

```

/tissue_type="Leaf"
/dev_stage="yellow Leaf With Greenish Base Area"
/lab_host="E. coli"
/clone_lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluescript SKII+;
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

```

## ORIGIN

Alignment Scores:

Pred. No.:	1.13e-31	Length:	435
Score:	298.00	Matches:	54
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-666-642-194\_COPY\_111\_164 (1-54) x CD529340 (1-435)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnLysArg 20  
 DB 215 GATGGTTTAAATGGAGGAAGTATGCAAGAAATCTGTCAAAAACAACATTAAACAAGAGG 274

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 DB 275 AATTACTACAATGCTCAAGTGAAGTCTCGGTGAAGAAGAGGTGATGAGATGATG 334

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 DB 335 GACGATCAGCTTATGATTACACATATGAGGAGTCCAT 376

## RESULT 2

LOCUS CB879380  
 DEFINITION HP11P20T HP Hordeum vulgare subsp. vulgare cDNA clone HP11P20  
 5-PRIME mRNA sequence.

ACCESSION CB879380  
 VERSION CB879380.1 GI:30081366

## KEYWORDS

SOURCE Hordeum vulgare subsp. vulgare

## ORGANISM

Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 643)

Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.

EST sequencing and analysis in barley (2002)

Unpublished (2002)

Contact: Stein Nils

Molecular Markers Group, Department Genbank

Institute of Plant Genetics and Crop Plant Research (IPK)

Correnstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522

Fax: 039482-5595

Email: stein@ipk-gatersleben.de

Insert length: 643 Std Error: 0.00

Plate: 11 row: P column: 20

Seq primer: T3.

## FEATURES

Location/Qualifiers

1..643

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="barke"

/sub\_species="vulgare"

/db\_xref="GABI:538869"

/db\_xref="taxon:112509"

/clone="HP11P20"

/tissue\_type="epidermis"

/dev\_stage="seedlings grown in greenhouse for 6 days"

/lab\_host="XL10-Gold"

```

/clone_lib="HP"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA). Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
850 bp"

```

## ORIGIN

Alignment Scores:

Pred. No.:	3.97e-25	Length:	643
Score:	253.00	Matches:	44
Percent Similarity:	90.74%	Conservative:	5
Best Local Similarity:	81.48%	Mismatches:	5
Query Match:	84.90%	Indels:	0
DB:	6	Gaps:	0

US-10-666-642-194\_COPY\_111\_164 (1-54) x CB879380 (1-643)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnLysArg 20  
 DB 482 GACGGCTACAAGTGGCGCAAGTACGCGCAAGAAAGTCCGTCAAGAACAGCCCAACCAAGG 541

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 DB 542 AACTACTACCGGTGCTCGACGGAAGGGTGCAGCGGTGAAGAAGCGGTGGCGGACCGG 601

QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 DB 602 GACGACCCCGGTACGTGCTGACCCACGTACGAGGGCACGCGAC 643

## RESULT 3

LOCUS AL503208  
 DEFINITION AL503208 Hordeum vulgare Barke roots Hordeum vulgare subsp. vulgare  
 cDNA clone HW01B17T 5', mRNA sequence.

ACCESSION AL503208  
 VERSION AL503208.1 GI:12029423

## KEYWORDS

SOURCE Hordeum vulgare subsp. vulgare

## ORGANISM

Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 700)

Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.

EST sequencing and analysis in barley

Unpublished (2000)

Contact: Michalek W

Institute for Plant Genetics and Crop Plant Research

Correnstr. 3, D-06466 Gatersleben, Germany

Email: michalek@ipk-gatersleben.de, http://pgcr.ipk-gatersleben.de

Seq primer: T3 primer for 5' end.

## FEATURES

Location/Qualifiers

1..700

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="barke"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HW01B17T"

/tissue\_type="roots"

/lab\_host="XL0LR"

/clone\_lib="Hordeum vulgare Barke roots"

/note="Vector: plasmid pBK-CMV; Site 1: EcoRI; Site 2:

XhoI; mRNA was made from roots of spring barley variety

'Barke', a high quality malting variety. Roots were grown

for two days on filter paper at room temperature. Cloning

sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).

NOTE: Due to a cloning artefact caused by the kit, in most





**VERSION** BI209002.1 GI:14686726  
**KEYWORDS** EST.  
**SOURCE** Lycopersicon esculentum (tomato)  
**ORGANISM** Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

**REFERENCE**  
**AUTHORS** 1 (bases 1 to 671)  
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,  
 Ronning, C. and Tanksley, S.  
**TITLE** Generation of ESTs from Tomato Suspension Cultures  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: CUGI  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>.

**FEATURES**  
 source  
 1..671  
 /location/Qualifiers  
 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA496, E6203"  
 /db\_xref="taxon:4081"  
 /clone="cTOS18r24"  
 /tissue\_type="suspension cultures"  
 /lab\_host="SOLR"  
 /clone\_lib="cTOS"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Suspension cultures of L.esculentum E6203 were grown in Murashige and Skoog based medium, supplemented with 1% coconut milk (filter sterilized and added after autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8). Fresh medium was added every 7 days, and cultures were grown at 25 C, with 12hrs of light and continuous shaking."

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 1..24 Length: 671  
 Score: 250.00 Matches: 44  
 Percent Similarity: 88.89% Conservative: 4  
 Best Local Similarity: 81.48% Mismatches: 6  
 Query Match: 83.89% Indels: 0  
 DB: 4 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x BI209002 (1-671)  
 Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg 20  
 Db 300 GATGGATTAAATGGAGGAATATGCAAAAGATGGTCAAGATAATCCAAATCCAAGG 359  
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 Db 360 AATTACTACAATGTTCAAGTGGGGGATGCAATGGAAGAAAGAGTAGAAGGACAAAT 419  
 Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 Db 420 AAGATTCAAGCTATGCTACTTACTTACTTATGAGGGATTCCAC 461

**RESULT 8**  
 BQ515840/c  
**LOCUS** BQ515840  
**DEFINITION** EST623255 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMU36 3', end, mRNA sequence.

**ACCESSION** BQ515840  
**VERSION** BQ515840.1  
**KEYWORDS** EST.  
**SOURCE** Solanum tuberosum (potato)  
**ORGANISM** Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

**REFERENCE**  
**AUTHORS** 1 (bases 1 to 412)  
 Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,  
 Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and  
 Karanycheva, S.A.  
**TITLE** Generation of a set of potato cDNA clones for microarray analyses  
**JOURNAL** Unpublished (2002)  
**COMMENT** Other ESTs: EST623254  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: [potato-array@tigr.org](mailto:potato-array@tigr.org)  
 This clone can be obtained from the University of Arizona Genomics  
 Institute. Orders can be made through URL:  
<http://genome.arizona.edu/orders/>  
 Seq primer: T7.

**FEATURES**  
 source  
 1..412  
 /location/Qualifiers  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec or Binjite"  
 /db\_xref="taxon:4113"  
 /clone="STMU36"  
 /tissue\_type="mixed tissues"  
 /lab\_host="SOLR"  
 /clone\_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"  
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."

**ORIGIN**  
 Alignment Scores:  
 Pred. No.: 8..47e-25 Length: 412  
 Score: 249.00 Matches: 43  
 Percent Similarity: 90.74% Conservative: 6  
 Best Local Similarity: 79.63% Mismatches: 5  
 Query Match: 83.56% Indels: 0  
 DB: 5 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x BQ515840 (1-412)  
 Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnLysArg 20  
 Db 406 GATGGATTAAATGGAGGAATATGCAAAAGATGGTCAAGATAATCCAAATCCAAGG 347  
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 Db 346 AATTACTACAATGTTCAAGTGGGAGGATGCAATGGAAGAAAGAGTAGAAGGACAAAT 287  
 Qy 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 Db 286 GAAGATTCAAGCTATGCTACTTACTTACTTATGAGGGATTCCAC 245

**RESULT 9**  
 BI433746  
**LOCUS** BI433746  
**DEFINITION** EST536507 P. infestans-challenged potato leaf, compatible reaction Solanum tuberosum cDNA clone PPCB103 5' sequence, mRNA sequence.

**ACCESSION** BI433746  
**VERSION** BI433746.1  
**KEYWORDS** EST.  
**SOURCE** Solanum tuberosum (potato)  
**ORGANISM** Solanum tuberosum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

**REFERENCE**  
**AUTHORS** 1 (bases 1 to 418)  
 Restrepo, S., Griffiths, H.M., Smart, C.D., Cho, J., Chiemiango, A.,  
 Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E. and Baker, B.  
**TITLE** Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction





Pred. No.: 1,07e-24 Length: 501  
 Score: 249.00 Matches: 44  
 Percent Similarity: 88.89% Conservatives: 4  
 Best Local Similarity: 81.48% Mismatches: 6  
 Query Match: 83.56% Indels: 0  
 DB: 4 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x BG049241 (1-501)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
 |||||  
 117 GATGATTCAATGGAGGAGTATGGGAAGAGGCTGTCAAGACAGCCCAATCCAAAGG 176  
 |||||  
 QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40  
 |||||  
 177 AACTACTACCGTGTCTGCGGAGGCGTCCGCGTGAAGAAGCGGTGGAGAGGACCGC 236  
 |||||  
 QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 |||||  
 237 GACGACCCCGCTACGTATCATCACCTACGACGCGGTCCAC 278  
 |||||

# RESULT 14

BE216050  
 LOCUS  
 DEFINITION HV\_CEB0009E04f Hordeum vulgare seedling green leaf EST library  
 HVCDA0005 (Blumeria challenged) Hordeum vulgare subsp. vulgare  
 CDNA clone HV\_CEB0009E04f, mRNA sequence.

ACCESSION BE216050  
 VERSION BE216050.1 GI:8903662

KEYWORDS  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Hordeum.

TITLE  
 JOURNAL 1 (bases 1 to 584)  
 COMMENT Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,  
 Friech, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J.,  
 Choi, D.W., Fenton, R.D., Oates, R. and Main, D.  
 Development of a genetically and physically anchored EST resource  
 for barley genomics: Blumeria infected incompatible (Mla6) seedling  
 leaf cDNA library  
 Unpublished (2001)

CONTACT: Wing RA  
 CLEMSON UNIVERSITY GENOMICS INSTITUTE  
 CLEMSON UNIVERSITY  
 100 JORDAN HALL, CLEMSON, SC 29634, USA  
 TEL: 864 656 7288  
 FAX: 864 656 4293  
 EMAIL: rwing@clermson.edu

TOTAL HQ BASES = 325  
 SEQ PRIMER: AATTACCTCTACTAAGGG  
 HIGH QUALITY SEQUENCE STOP: 556.

## FEATURES

source  
 1..584  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Cil16151 (Mla6)"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HV\_CEB0009E04f"  
 /tissue\_type="seedling green leaf"  
 /lab\_host="SOLR"  
 /clone\_lib="Hordeum vulgare seedling green leaf EST  
 library HVCDA0005 (Blumeria challenged)"  
 /note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;  
 C.I. 16151 (Mla6) plants were greenhouse grown in the R  
 Wise lab at Iowa State University, Ames, IA; 7 day old  
 green seedlings were challenged with isolate 5874  
 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves  
 were harvested 20 and 24 hr post-inoculation and snap  
 frozen; uninoculated leaves were harvested 20 hr  
 post-inoculation (Wei, Wise). In the TJ Close lab at the

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,29e-24 Length: 584  
 Score: 249.00 Matches: 43  
 Percent Similarity: 88.89% Conservatives: 5  
 Best Local Similarity: 79.83% Mismatches: 6  
 Query Match: 83.56% Indels: 0  
 DB: 2 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x BE216050 (1-584)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
 |||||  
 377 GACGCTACAAAGTGGCGCAAGTACGCGCAAGAAAGTCGTCACAGACAGCCCAACCCAAAGG 436  
 |||||  
 QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysArgValGluArgAspGly 40  
 |||||  
 437 AACTACTACCGTGTCTGCGGAGGCGTCCGACGTGAAGAGCGGTGGAGCGGACCGG 496  
 |||||  
 QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 |||||  
 497 GACGATCCGGCGTACGTGGTACCACCGTACGAGGCGCACGCAC 538  
 |||||

## RESULT 15

BM328984

LOCUS

DEFINITION

BM328984

ACCESSION

BM328984

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM328984 610 bp mRNA linear EST 04-JAN-2002  
 PIC1\_31\_H12-gl\_A002 Pathogen-infected compatible 1 (PIC1) Sorghum  
 bicolor cDNA, mRNA sequence.  
 BM328984 GI:18068121  
 Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 610)  
 Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Dean, R., Wing, R.,  
 Sudman, M. and Pratt, L.H.  
 An EST database from Sorghum: plants infected with a compatible  
 pathogen  
 Unpublished (2002)  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Sequences have been trimmed to exclude PolyA, vector, and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20. Three-prime sequences, which are obtained with PolyTWix or

University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Friech, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Friech, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

T7 sequencing primer, are presented as the reverse complement.

Seq primer: T7  
High quality sequence start: 20  
High quality sequence stop: 610  
POLVA=Yes.

# FEATURES

source Location/Qualifiers  
1..610  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/tissue\_type="Leaves"  
/dev\_stage="4-week-old seedlings infected with Colletotrichum graminicola"  
/clone\_lib="Pathogen-infected compatible 1 (PIC1)"  
/note="Vector: pBluescript II SK(-) from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum seedlings were sprayed with spore suspension prepared from 3-week-old FRM421, a sorghum isolate of the anthracnose pathogen Colletotrichum graminicola. Inoculated plants were kept in a 25 C dark growth chamber with 100% relative humidity for 24 hr, followed by 12/12 hr of light/dark cycle at 25 C with 90% relative humidity for another 24 hr. All leaves were harvested and quick frozen with liquid nitrogen and stored in a -80 C freezer. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from the pathogen."

# ORIGIN

Alignment Scores:  
Pred. No.: 1.36e-24 Length: 610  
Score: 249.00 Matches: 44  
Percent Similarity: 88.89% Conservative: 4  
Best Local Similarity: 81.48% Mismatches: 6  
Query Match: 83.56% Indels: 0  
DB: 4 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x BM328984 (1-610)

Qy 1 AspGlyPheLysTrrArgLysTrrGlyLysLysSerValLysAsnAsnIleAsnLysArg 20  
Db 133 GATGGATTCAATGGAGGAAGTATGGGAAGAGGCTGTCAAGAACAGCCCAATCCAAGG 192  
Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
Db 193 AACTACTACCGCTGCTCGTGGAGGGCTGCGGCGTGAAGAGCGGGTGGAGAGGACCGC 252  
Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
Db 253 GACGACCCCGCGTAGTGTATCACCACCTACGACGGCGTCCAC 294

Search completed: August 26, 2005, 01:46:02  
Job time : 2312 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 25, 2005, 18:08:19 ; Search time 391 Seconds  
(without alignments)

817.560 Million cell updates/sec

Title: US-10-666-642-194\_COPY\_111\_164

Perfect score: 298

Sequence: 1 DGFKRWKYGKSKVNINKR.....RVERDGDAAAYVITTYEGVH 54

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPRO\_spool/US10666642/runat\_25082005\_130052\_24846/app\_query.fasta\_1.199  
-DB=N Geneseq\_16Dec04 -QMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10666642 @CGN 1.1 644 @runat\_25082005\_130052\_24846 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	100.0	585	12 ADO02392	Ado02392 Thalecres
2	298	100.0	585	12 ADO61726	Ado61726 Thalecres
3	298	100.0	1917	3 AAC49725	Aac49725 Arabidops
4	250	83.9	740	12 ADO63551	Ado63551 Thalecres
5	249	83.6	823	12 ADO03201	Ado03201 Corn orth

6	249	83.6	823	12 ADO62507	Ado62507 Thalecres
7	249	83.6	1663	12 ADI43068	Adi43068 Plant tra
8	249	83.6	1663	12 ADO03208	Ado03208 Corn orth
9	248	83.2	680	12 ADO03200	Ado03200 Corn orth
10	248	83.2	680	12 ADO62506	Ado62506 Thalecres
11	248	83.2	743	12 ADO03199	Ado03199 Corn orth
12	248	83.2	743	12 ADO62505	Ado62505 Thalecres
13	247	82.9	974	12 ADO03196	Ado03196 Soybean o
14	247	82.9	974	12 ADO62502	Ado62502 Thalecres
15	244	81.9	1696	12 ADI43067	Adi43067 Plant tra
16	244	81.9	1696	12 ADO03207	Ado03207 Corn orth
17	243	81.5	834	12 ADO03202	Ado03202 Corn orth
18	243	81.5	834	12 ADO62508	Ado62508 Thalecres
19	242	81.2	825	12 ADI43066	Adi43066 Plant tra
20	242	81.2	825	12 ADO03203	Ado03203 Rice orth
21	239	80.2	1235	12 ADO03195	Ado03195 Soybean o
22	239	80.2	1235	12 ADO62501	Ado62501 Thalecres
23	232	77.9	999	12 ADI43069	Adi43069 Plant tra
24	232	77.9	999	12 ADO03209	Ado03209 Corn orth
25	230	77.2	748	6 ABK65246	ABK65246 Arabidops
26	230	77.2	748	9 ACD98373	ACD98373 A. thalia
27	230	77.2	748	10 ADD29972	Add29972 Plant yie
28	230	77.2	748	12 ADI41790	Adi41790 Plant tra
29	230	77.2	748	12 ADO02394	Ado02394 Thalecres
30	197	66.1	444	3 AAC45051	Aac45051 Arabidops
31	197	66.1	548	3 AAC35279	Aac35279 Arabidops
32	197	66.1	569	3 AAC48380	Aac48380 Arabidops
33	197	66.1	624	3 AAC38694	Aac38694 Arabidops
34	197	66.1	724	9 ADA15508	Ada15508 DNA encod
35	197	66.1	724	9 ACD98365	ACD98365 A. thalia
36	197	66.1	724	12 ADO01672	Ado01672 Thalecres
37	197	66.1	1306	10 ADD31000	Add31000 Plant yie
38	197	66.1	1306	12 ADI44148	Adi44148 Plant tra
39	197	66.1	1306	12 ADO61750	Ado61750 Thalecres
40	195	65.4	1182	6 ABZ13876	Abz13876 Arabidops
41	195	65.4	1182	8 ADA68247	Ada68247 Arabidops
42	195	65.4	1398	9 ADA15532	Ada15532 DNA encod
43	195	65.4	1398	12 ADO01670	Ado01670 Thalecres
44	195	65.4	1462	9 ADB23121	Adb23121 Environme
45	195	65.4	1589	3 AAC40213	Aac40213 Arabidops

ALIGNMENTS

RESULT 1

ADO02392

ID ADO02392 standard; cDNA; 585 BP.

XX ADO02392;

XX 01-JUL-2004 (first entry)

XX Thalecres transcription factor cDNA #403.

XX Thalecres; transcription factor; ss, gene; plant; transgenic;  
XX abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;  
XX phosphate limitation; potassium limitation; nitrogen limitation;  
XX hormone sensitivity; disease resistance; sugar sensing; seed germination;  
XX flowering; inflorescence architectural change;  
XX meristem cell differentiation; phyllotaxy; apical dominance;  
XX trichome development; seed development; premature senescence;  
XX delayed senescence; lethality; necrosis; plant size; leaf morphology;  
XX seed morphology; secondary metabolism; light response; shade avoidance.

XX Arabidopsis thaliana.

XX US2004045049-A1.

XX 04-MAR-2004.

XX 10-APR-2003; 2003US-00412699.

XX 13-SEP-1999; 99US-00394519.

PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533028.  
 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000WO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 17-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 XX Zhang J, Fromm ME, Riechmann JL, Adam LJ, Broun PE;  
 PI Pineda O, Reuber TL, Keddle JS, Yu G, Jiang C, Samaha RS;  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;  
 PI Sherman BK;  
 XX WPI: 2004-225755/21.  
 DR P-PSDB; ADO02393.  
 XX New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 PT Claim 1; SEQ ID NO 805; 213pp; English.  
 PS The invention relates to a transgenic plant comprising a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to

CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced  
 CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered stem development, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenly lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, an alteration of leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an increase in seed oil content, decrease in seed oil  
 CC biochemistry, an increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenly lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes a  
 CC thalacress transcription factor of the invention.  
 XX

SQ Sequence 585 BP; 202 A; 95 C; 135 G; 153 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5, 9e-34 Length: 585  
 Score: 298.00 Matches: 54  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO02392 (1-585)

Qy 1 AspGlyPheLysTrpArgLysTyrglyLysSerVallyAsnAsnIleAsnLysArg 20  
 |||||  
 Db 331 GATGGTTTAAATCGAGGAGTATGGCAAGAAATCTGTCAAAAACACATTAACAAGAGG 390  
 |||||  
 Qy 21 AsnTyrrTyrrLysCysSerSerGluGlyCysSerVallyLysArgValGluArgAspGly 40  
 |||||  
 Db 391 AATTACTACAAATGCTCAAGTGAAGGTTGCTCGGTGAAGAGGCTAGAGAGATGGT 450  
 |||||  
 Qy 41 AspAspAlaAlaTyrrValIleThrThrTyrrGluGlyValHis 54  
 |||||  
 Db 451 GACGATGCAGCTTATGTAAATTACACATATGACGAGGATCCAT 492  
 |||||

RESULT 2

ADO61726  
 ID ADO61726 standard; DNA; 585 BP.

AC ADO61726;

XX 15-JUL-2004 (first entry)

Transcription factor G1274 coding sequence, SEQ ID 193.

KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KW osmotic stress tolerance; cold tolerance; heat tolerance;  
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KW glyphosate resistance; flowering; fertility; seed development; ds.  
 OS Arabidopsis thaliana.

FN WO2004031349-A2.

XX 15-APR-2004.

XX 18-SEP-2003; 2003WO-US030292.  
XX 18-SEP-2002; 2002US-0411837P.  
XX 17-DEC-2002; 2002US-0434156P.  
XX 24-APR-2003; 2003US-0465809P.  
XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
XX Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;  
XX WPI; 2004-330163/30.  
XX P-ESDB; ADO61727.  
XX New recombinant polynucleotide encoding transcription factor  
XX polypeptides, useful for producing transgenic plants with advantageous  
XX properties compared to a reference plant.  
XX Claim 1; SEQ ID NO 193; 510pp; English.  
XX The present invention relates to novel plant transcription factor  
XX proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
XX sequences can be used to produce transgenic plants, which overexpress  
XX (II), where the transgenic plant has an altered trait as compared to a  
XX non-transgenic plant or wild-type plant. The transgenic plant comprises  
XX an altered trait selected from increased tolerance to abiotic stress,  
XX increased tolerance to osmotic stress, increased tolerance to cold,  
XX increased germination in cold, increased tolerance to heat, increased  
XX germination in heat, increased tolerance to freezing conditions,  
XX increased tolerance to low nitrogen conditions, increased tolerance to  
XX low phosphate conditions, increased tolerance to disease, including  
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
XX increased tolerance to multiple fungal pathogens, increased resistance to  
XX glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
XX increased sensitivity to ACC, altered sugar sensing, increased tolerance  
XX to sugars, altered carbon/nitrogen sensing, early flowering, late  
XX flowering, altered flower meristem development, altered branching pattern,  
XX fertility, altered shoot meristem development, altered branching pattern,  
XX altered stem morphology, altered vascular tissue structure, reduced  
XX apical dominance, altered trichome density, altered trichome development,  
XX altered trichome structure, altered root development, altered shade  
XX avoidance, altered seed development, altered seed ripening, altered seed  
XX germination, slow growth, fast growth, altered cell differentiation,  
XX altered cell proliferation, altered cell expansion, altered phase change,  
XX altered senescence, abnormal embryo development, altered programmed cell  
XX death, lethality when overexpressed, altered necrosis patterns, increased  
XX plant size, increased biomass, large seedlings, dwarfed plants, dark  
XX green leaves, change in leaf shape, increased leaf size and mass, light  
XX green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
XX altered seed coloration, altered seed size, altered seed shape, large  
XX seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
XX content, altered seed protein content, altered seedprenyl content,  
XX altered leaf prenyl lipid content, increased anthocyanin levels, and  
XX decreased anthocyanin levels. Note: The sequence data for this patent did  
XX not form part of the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 585 BP; 202 A; 95 C; 135 G; 153 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 5,9e-34 Length: 585  
Score: 298.00 Matches: 54  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO61726 (1-585)  
Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnLysArg 20  
|||||

Db 331 GATGGTTTTAAATGGAGGAAGTATGGCAAGAAATCTGTCAAAACACATTAAACAAGAGG 390  
Qy 21 AsnTyrTrpLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40  
|||||  
Db 391 AATTACTACAAATGCTCAAGTGAAGGTTGCTCGGTGAAGAAGAGGGGTAGAGAGATGGT 450  
Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
|||||  
Db 451 GACGATGCAGCTTATGTATTAATTAACAACATATGAAGAGTCCAT 492  
RESULT 3  
AAC49725  
ID AAC49725 standard; DNA; 1917 BP.  
XX  
AC AAC49725;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62208.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 29-MAR-1999; 99US-0126264P.  
PR 01-APR-1999; 99US-0126785P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999;	99US-0138847P;	PR 10-AUG-1999;	99US-0148171P;
PR 14-JUN-1999;	99US-0139119P;	PR 11-AUG-1999;	99US-0148319P;
PR 16-JUN-1999;	99US-0139452P;	PR 12-AUG-1999;	99US-0148341P;
PR 16-JUN-1999;	99US-0139453P;	PR 13-AUG-1999;	99US-0148565P;
PR 17-JUN-1999;	99US-0139492P;	PR 13-AUG-1999;	99US-0148684P;
PR 18-JUN-1999;	99US-0139454F;	PR 16-AUG-1999;	99US-0149368P;
PR 18-JUN-1999;	99US-0139455P;	PR 17-AUG-1999;	99US-0149175P;
PR 18-JUN-1999;	99US-0139456P;	PR 18-AUG-1999;	99US-0149436P;
PR 18-JUN-1999;	99US-0139457P;	PR 20-AUG-1999;	99US-0149722P;
PR 18-JUN-1999;	99US-0139458P;	PR 20-AUG-1999;	99US-0149723P;
PR 18-JUN-1999;	99US-0139459P;	PR 20-AUG-1999;	99US-0149929P;
PR 18-JUN-1999;	99US-0139460P;	PR 23-AUG-1999;	99US-0149902P;
PR 18-JUN-1999;	99US-0139461P;	PR 23-AUG-1999;	99US-0149930P;
PR 18-JUN-1999;	99US-0139462P;	PR 25-AUG-1999;	99US-0150566P;
PR 18-JUN-1999;	99US-0139463P;	PR 26-AUG-1999;	99US-0150884P;
PR 18-JUN-1999;	99US-0139750P;	PR 27-AUG-1999;	99US-0151065P;
PR 18-JUN-1999;	99US-0139763P;	PR 27-AUG-1999;	99US-0151066P;
PR 21-JUN-1999;	99US-0139817P;	PR 27-AUG-1999;	99US-0151080P;
PR 22-JUN-1999;	99US-0139899P;	PR 30-AUG-1999;	99US-0151303P;
PR 23-JUN-1999;	99US-0140353P;	PR 31-AUG-1999;	99US-0151438P;
PR 23-JUN-1999;	99US-0140354P;	PR 01-SEP-1999;	99US-0151930P;
PR 24-JUN-1999;	99US-0140695P;	PR 07-SEP-1999;	99US-0152363P;
PR 28-JUN-1999;	99US-0140823P;	PR 10-SEP-1999;	99US-0153070P;
PR 29-JUN-1999;	99US-0140991P;	PR 13-SEP-1999;	99US-0153758P;
PR 30-JUN-1999;	99US-0141287P;	PR 15-SEP-1999;	99US-0154018P;
PR 01-JUL-1999;	99US-0141842P;	PR 16-SEP-1999;	99US-0154039P;
PR 01-JUL-1999;	99US-0142154P;	PR 20-SEP-1999;	99US-0154779P;
PR 02-JUL-1999;	99US-0142055P;	PR 22-SEP-1999;	99US-0155139P;
PR 06-JUL-1999;	99US-0142390P;	PR 23-SEP-1999;	99US-0155486P;
PR 08-JUL-1999;	99US-0142803P;	PR 24-SEP-1999;	99US-0155659P;
PR 09-JUL-1999;	99US-0142920P;	PR 28-SEP-1999;	99US-0156458P;
PR 12-JUL-1999;	99US-0142977P;	PR 29-SEP-1999;	99US-0156596P;
PR 13-JUL-1999;	99US-0143542P;	PR 04-OCT-1999;	99US-0157117P;
PR 14-JUL-1999;	99US-0143624P;	PR 05-OCT-1999;	99US-0157753P;
PR 15-JUL-1999;	99US-0144005P;	PR 06-OCT-1999;	99US-0157865P;
PR 16-JUL-1999;	99US-0144085P;	PR 07-OCT-1999;	99US-0158029P;
PR 16-JUL-1999;	99US-0144086P;	PR 08-OCT-1999;	99US-0158232P;
PR 19-JUL-1999;	99US-0144325P;	PR 12-OCT-1999;	99US-0158369P;
PR 19-JUL-1999;	99US-0144331P;	PR 13-OCT-1999;	99US-0159293P;
PR 19-JUL-1999;	99US-0144332P;	PR 13-OCT-1999;	99US-0159294P;
PR 19-JUL-1999;	99US-0144333P;	PR 13-OCT-1999;	99US-0159295P;
PR 19-JUL-1999;	99US-0144334P;	PR 14-OCT-1999;	99US-0159329P;
PR 19-JUL-1999;	99US-0144335P;	PR 14-OCT-1999;	99US-0159330P;
PR 20-JUL-1999;	99US-0144352P;	PR 14-OCT-1999;	99US-0159331P;
PR 20-JUL-1999;	99US-0144632P;	PR 14-OCT-1999;	99US-0159637P;
PR 20-JUL-1999;	99US-0144884P;	PR 14-OCT-1999;	99US-0159638P;
PR 21-JUL-1999;	99US-0144814P;	PR 18-OCT-1999;	99US-0159584P;
PR 21-JUL-1999;	99US-0145086P;	PR 21-OCT-1999;	99US-0160741P;
PR 21-JUL-1999;	99US-0145088P;	PR 21-OCT-1999;	99US-0160767P;
PR 22-JUL-1999;	99US-0145085P;	PR 21-OCT-1999;	99US-0160768P;
PR 22-JUL-1999;	99US-0145087P;	PR 21-OCT-1999;	99US-0160770P;
PR 22-JUL-1999;	99US-0145089P;	PR 21-OCT-1999;	99US-0160814P;
PR 22-JUL-1999;	99US-0145192P;	PR 21-OCT-1999;	99US-0160815P;
PR 23-JUL-1999;	99US-0145145P;	PR 22-OCT-1999;	99US-0160980P;
PR 23-JUL-1999;	99US-0145218P;	PR 22-OCT-1999;	99US-0160981P;
PR 23-JUL-1999;	99US-0145218P;	PR 22-OCT-1999;	99US-0160989P;
PR 26-JUL-1999;	99US-0145276P;	PR 25-OCT-1999;	99US-0161404P;
PR 27-JUL-1999;	99US-0145913P;	PR 25-OCT-1999;	99US-0161405P;
PR 27-JUL-1999;	99US-0145918P;	PR 25-OCT-1999;	99US-0161406P;
PR 27-JUL-1999;	99US-0145919P;	PR 26-OCT-1999;	99US-0161359P;
PR 28-JUL-1999;	99US-0145951P;	PR 26-OCT-1999;	99US-0161360P;
PR 02-AUG-1999;	99US-0146386P;	PR 26-OCT-1999;	99US-0161361P;
PR 02-AUG-1999;	99US-0146388P;	PR 28-OCT-1999;	99US-0161920P;
PR 02-AUG-1999;	99US-0146389P;	PR 28-OCT-1999;	99US-0161922P;
PR 03-AUG-1999;	99US-0147038P;	PR 28-OCT-1999;	99US-0161993P;
PR 04-AUG-1999;	99US-0147204P;	PR 29-OCT-1999;	99US-0162142P;
PR 04-AUG-1999;	99US-0147302P;		
PR 05-AUG-1999;	99US-0147192P;		
PR 06-AUG-1999;	99US-0147360P;		
PR 06-AUG-1999;	99US-0147303P;		
PR 06-AUG-1999;	99US-0147416P;		
PR 09-AUG-1999;	99US-0147493P;		
PR 09-AUG-1999;	99US-0147935P;		

Alignment Scores:

Pred. No.:

2.84e-33

Score:

298.00

Percent Similarity:

100.00%

Best Local Similarity:

100.00%

Query Match:

100.00%

Length:

1917

Matches:

54

Conservative:

0

Mismatches:

0

Indels:

0

DB: 3 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x AAC49725 (1-1917)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAenLysArg 20  
 |||||  
 331 GATGGTTTAAATGGAGAAATATGGCAAGAAATCTGTCAAAACAACATTAACAGAGG 390

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 |||||  
 391 AATTACTACAAATCTCAAGTGAAGGTTGCTCGGTGAAGAAGAGGGTAGAGAGATGGT 450

QY 41 AspAspAlaLalaTyrValLleThrTyrGluGlyValHis 54  
 |||||  
 451 GACGATGCAGCTTATGTATTAATACAAACATATCAGAGGAGTCCAT 492

RESULT 4  
 ADO63551/C  
 ID ADO63551 standard; DNA; 740 BP.  
 XX  
 AC ADO63551;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Transcription factor G1274 orthologous sequence, SEQ ID 2018.  
 XX  
 KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KW osmotic stress tolerance; cold tolerance; heat tolerance;  
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KW glyphosate resistance; flowering; fertility; seed development; ds.  
 XX  
 OS Lycopersicon esculentum.  
 XX  
 PN WO2004031349-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 18-SEP-2003; 2003WO-US030292.  
 XX  
 PR 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-0465809P.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
 PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;  
 XX  
 DR WPI; 2004-330163/30.  
 XX  
 PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 XX  
 PS Claim 1; SEQ ID NO 2018; 510pp; English.  
 XX  
 CC The present invention relates to novel plant transcription factor  
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (II), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stress,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced

CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprenyl content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 740 BP; 229 A; 131 C; 114 G; 266 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. No.: 8.78e-27 Length: 740  
 Score: 250.00 Matches: 44  
 Percent Similarity: 88.89% Conservative: 4  
 Best Local Similarity: 81.48% Mismatches: 6  
 Query Match: 83.89% Indels: 0  
 DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO63551 (1-740)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAenLysArg 20  
 |||||  
 435 GATGGTTTAAATGGAGAAATATGGCAAGAAATGTCAGATTAATCCAAATCCAAGG 376

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 |||||  
 375 AATTACTACAAATGTTCAAGTGGGGATGCAATGTGAAGAAAGAGTAGAAGGACAAAT 316

QY 41 AspAspAlaLalaTyrValLleThrTyrGluGlyValHis 54  
 |||||  
 315 AAAGATTCAAGCTATGTCATTACTATTATGAAGGGGATTCCAC 274

DB  
 RESULT 5  
 ID ADO03201  
 XX  
 AC ADO03201;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Corn orthologue of Thalecress transcription factor, cDNA #180.  
 XX  
 KW Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;  
 KW cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phyllotaxy; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.  
 XX  
 OS Zea mays.  
 XX  
 PN US2004045049-A1.  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 10-APR-2003; 2003US-00412699.  
 XX

PR 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533029.  
 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 16-APR-2000; 2000WO-US009448.  
 PR 06-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PILG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 XX  
 PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;  
 PI Sherman BK;  
 XX  
 WPI; 2004-225755/21.  
 XX  
 PT New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 XX  
 PS Claim 1; SEQ ID NO 1615; 213pp; English.  
 XX  
 CC The invention relates to a transgenic plant comprises a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to

CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced  
 CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered seed development, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenly lipid  
 CC content, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC sugars, an alteration of leaf glucosinolate content, change in seed  
 CC content, an increase in seed oil content, decrease in seed oil  
 CC biochemistry, an increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed fatty acid content, decrease in seed protein  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenly lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes an  
 CC orthologue of a thalacress transcription factor isolated from Corn.  
 XX  
 SQ Sequence 823 BP; 172 A; 258 C; 247 G; 144 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1,42e-26 Length: 823  
 Score: 249.00 Matches: 44  
 Percent Similarity: 88.89% Conservative: 4  
 Best Local Similarity: 81.48% Mismatches: 6  
 Query Match: 83.56% Indels: 0  
 DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO03201 (1-823)

Oy 1 AspGlyPheLysTrpArgLysTyrgLysLysSerValLysAsnAsnLysArg 20  
 Db 441 GACGGATTCAAGTGGAGGAGTACGGGAAGAAGCGCTCAAGAAGACAGCCCAATCCAAAGG 500  
 Oy 21 AsnTyTyTyLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 Db 501 AACTACTACCGCTGCTGCTGGAGGGCTGCGCGGTGAAGAAGCGGTGGAGAGGACCGC 560  
 Oy 41 AspAspAlaAlaIatyrValIleThrThrTyrgLysValHis 54  
 Db 561 GACGACCCCGCTAGCTCATCCACCCTACGACGGCGTCCAC 602

RESULT 6  
 ADO62507

ID ADO62507 standard; DNA; 823 BP.

AC ADO62507;

XX 15-JUL-2004 (first entry)

XX Transcription factor G1274 orthologous sequence, SEQ ID 974.

KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KW osmotic stress tolerance; cold tolerance; heat tolerance;  
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KW glyphosate resistance; flowering; fertility; seed development; ds.  
 OS Zea mays.

PN WO2004031349-A2.

XX 15-APR-2004.

XX 18-SEP-2003; 2003WO-US030292.  
 XX 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-0465809P.  
 XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
 PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;  
 XX WPI; 2004-330163/30.  
 XX New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 XX Claim 1; SEQ ID NO 974; 510pp; English.  
 XX The present invention relates to novel plant transcription factor  
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (II), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stress,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Bysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprenyl content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 823 BP; 172 A; 258 C; 247 G; 144 T; 0 U; 2 Other;  
 Alignment Scores:  
 Pred. No.: 1.42e-26 Length: 823  
 Score: 249.00 Matches: 44  
 Percent Similarity: 88.99% Conservative: 4  
 Best Local Similarity: 81.48% Mismatches: 6  
 Query Match: 83.56% Indels: 0  
 DB: 12 Gaps: 0  
 US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO62507 (1-823)  
 Qy 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysArgValGluArgAspGly 20  
 Db 441 GACGGATTCAAGTGAGGAGTAGTCGGGAAGAGCGGCTCAAGAACAGCCCAATCCARGG 500

Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 Db 501 AACTACTACGCTGCTCGTGGAGGGCTGGGCGCTGAAGAGCGGTTGGAGAGGCGCGC 560  
 Qy 41 AspAspAlaAlaTyrValIleThrThrTyrGluGlyValHis 54  
 Db 561 GAGGACCCCGCTACGTACATCACCACCTACGACGGCGTCCAC 602

RESULT 7  
 ID ADI43068  
 XX ADI43068 standard; DNA; 1663 BP.  
 AC ADI43068;  
 XX 22-APR-2004 (first entry)  
 XX Plant transcription factor polynucleotide #1006.  
 DE transgenic; plant; enhanced tolerance to abiotic stress;  
 KW glycosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; gene; ds.  
 XX Zea mays.  
 XX US2004019927-A1.  
 XX 29-JAN-2004.  
 XX 25-FEB-2003; 2003US-00374780.  
 XX 18-APR-2001; 2001US-00837944.  
 XX (SHER/) SHERMAN B K.  
 XX (RIEC/) RIECHMANN J L.  
 XX (JIANG/) JIANG C.  
 XX (HEAR/) HEARD J E.  
 XX (HAAK/) HAAKE V.  
 XX (CREE/) CREELMAN R A.  
 XX (RATC/) RATCLIFFE O.  
 XX (ADAM/) ADAM L J.  
 XX (REUB/) REUBER T L.  
 XX (KEDD/) KEDDIE J.  
 XX (BROU/) BROUN P E.  
 XX (PILG/) PILGRIM M L.  
 XX (DUBE/) DUBELL A N.  
 XX (PINE/) PINEDA O.  
 XX (YUGG/) YU G.  
 XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;  
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;  
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 XX WPI; 2004-132245/13.  
 XX New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX Claim 1; SEQ ID NO 1531; 435pp; English.  
 XX The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glycosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;

CC altered flower structure, change in stem bifurcations, altered branching  
 CC pattern, reduced apical dominance, reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This sequence represents a thaliana  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.

XX SQ Sequence 1663 BP; 417 A; 453 C; 494 G; 299 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	3 6e-26	Length:	1663
Score:	249.00	Matches:	44
Percent Similarity:	88.8%	Conservative:	4
Best Local Similarity:	81.4%	Mismatches:	6
Query Match:	83.56%	Indels:	0
DB:	12	Gaps:	0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADI43068 (1-1663)

QY 1 AspGlyPheLysTyrArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
 |||||  
 1078 GACGGATTCACTGAGGAGGAGTACGGGAAGAGGCGTCAAGACAGCCCAATCCAAGG 1137  
 |||||  
 QY 21 AenTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 |||||  
 1138 AACTACTACCGTCTGCTGTCGGAGGCGTCGCGCGTGAAGAACGGGTGGAGAGGACCGC 1197  
 |||||  
 QY 41 AspAspAlaAlaTyrValIleThrTyrGluGlyValHis 54  
 |||||  
 1198 GACGACCCCGCTACGTATCATCACCTACGACGCGGTCCAC 1239  
 |||||

#### RESULT 8

ID ADO03208 standard; cDNA; 1663 BP.  
 XX AC ADO03208;  
 XX DT 01-JUL-2004 (first entry)  
 XX DE Corn orthologue of Thalecress transcription factor, cDNA #183.  
 KW Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;  
 KW cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phyllotaxy; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.  
 OS Zea mays.  
 XX PN US2004045049-A1.  
 XX PD 04-MAR-2004.  
 XX PF 10-APR-2003; 2003US-00412699.  
 XX PR 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
 PR 22-MAR-2000; 2000US-00533029.

PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000WO-US009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 17-DEC-2002; 2002US-00225068.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX (ZHAN//) ZHANG J.  
 PA (FROM//) FROMM M E.  
 PA (HEAR//) HEARD J E.  
 PA (RIEC//) RIECHMANN J L.  
 PA (ADAM//) ADAM L J.  
 PA (BROU//) BROUN P E.  
 PA (PINE//) PINEDA O.  
 PA (REUB//) REUBER T L.  
 PA (KEDD//) KEDDIE J S.  
 PA (YUGG//) YU G.  
 PA (JIAN//) JIANG C.  
 PA (SAMA//) SAMAHA R S.  
 PA (PILG//) PILGRIM M L.  
 PA (CREE//) CREELMAN R A.  
 PA (DUBE//) DUBELL A N.  
 PA (RATC//) RATCLIFFE O.  
 PA (KUMI//) KUMIMOTO R.  
 PA (SHER//) SHERMAN B K.  
 XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;  
 PI Pineda O, Reuber TU, Keddie JS, Yu G, Jiang C, Samaha RS;  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;  
 PI Sherman BK;  
 DR WPI; 2004-225755/21.  
 XX New transgenic plant, useful in developing phenotypes with altered or  
 PT improved characteristics or traits.  
 PS Claim 1; SEQ ID NO 1622; 213pp; English.  
 CC The invention relates to a transgenic plant comprises a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
 CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in



CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Bryopsis, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Scierotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phylloclax, altered branching pattern, reduced  
 CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered stem morphology, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an alteration of leaf glucosinolate content, change in seed  
 CC biochemistry, an increase in seed oil content, decrease in seed oil  
 CC content, increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, increase in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenyl lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence encodes an  
 CC orthologue of a thalacress transcription factor isolated from Corn.  
 XX  
 SQ Sequence 680 BP; 129 A; 206 C; 213 G; 132 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.54e-26 Length: 680  
 Score: 248.00 Matches: 42  
 Percent Similarity: 92.59% Conservative: 8  
 Best Local Similarity: 77.78% Mismatches: 4  
 Query Match: 83.22% Indels: 0  
 DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO03200 (1-680)

Qy 1 AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAenLysArg 20  
 Db 57 GACGGTACAGTGGAGGAGTACGCGACAGAGTCCGTCAAGACAGCCCCAACCAAGG 116  
 Qy 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly 40  
 Db 117 AACTACTACCGGTGCTCGACGGAGGGTGCAACGTGAGAACGGGTGGAGCGGACCAAG 176  
 Qy 41 AspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54  
 Db 177 GACGACCCACGACTACGTGTGTGACGACGTACGAGGGGGATGCAC 218

RESULT 10

ADO62506

ID ADO62506 standard; DNA; 680 BP.

XX

AC ADO62506;

XX 15-JUL-2004 (first entry)

DE Transcription factor G1274 orthologous sequence, SEQ ID 973.

XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KW osmotic stress tolerance; cold tolerance; heat tolerance;  
 KW low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KW glyphosate resistance; flowering; fertility; seed development; ds.  
 XX  
 OS Zea mays.

PN WO2004031349-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 18-SEP-2003; 2003WO-US030292.  
 XX  
 PR 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-045809P.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
 PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;  
 XX  
 DR WPI; 2004-330163/30.  
 XX  
 PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 XX  
 PS Claim 1; SEQ ID NO 973; 510pp; English.  
 XX

The present invention relates to novel plant transcription factor  
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (II), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stress,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprenyl content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 680 BP; 129 A; 206 C; 213 G; 132 T; 0 U; 0 Other;

Alignment Scores:

Score: 1.54e-26 Length: 680  
 Pred. No.: 248.00 Matches: 42  
 Percent Similarity: 92.59% Conservative: 8  
 Best Local Similarity: 77.78% Mismatches: 4  
 Query Match: 83.22% Indels: 0  
 DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO62506 (1-680)



Score: 248.00 Matches: 42  
Percent Similarity: 92.59% Conservative: 8  
Best Local Similarity: 77.78% Mismatches: 4  
Query Match: 83.22% Indels: 0  
DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO03199 (1-743)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
DB 18 GACGGCTACAGTGGAGGAGTACGGCAAGAGTCCGTCAAGAACAGCCCCAACCAAGG 77

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40  
DB 78 AACTACTACCGTGTCTCGACGGAAGGGTCAACGTGAGAGCGGGTGGAGCGGACCAAG 137

QY 41 AspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54  
DB 138 GACGACCCAGCTACGTGTGACGAGTACGAGGGGATGCAC 179

RESULT 12  
ADO62505  
ID ADO62505 standard; DNA; 743 BP.  
XX AC ADO62505;  
XX DT 15-JUL-2004 (first entry)  
XX DE Transcription factor G1274 orthologous sequence, SEQ ID 972.  
XX KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
KW osmotic stress tolerance; cold tolerance; heat tolerance;  
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;  
KW glyphosate resistance; flowering; fertility; seed development; ds.  
XX OS Zea mays.  
XX PN WO2004031349-A2.  
XX PD 15-APR-2004.  
XX PF 18-SEP-2003; 2003WO-US030292.  
XX PR 18-SEP-2002; 2002US-0411837P.  
XX PR 17-DEC-2002; 2002US-0434166P.  
XX PR 24-APR-2003; 2003US-0465809P.  
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;  
XX WPI; 2004-330163/30.  
XX PT New recombinant polynucleotide encoding transcription factor  
PT polypeptides, useful for producing transgenic plants with advantageous  
PT properties compared to a reference plant.  
XX PS Claim 1; SEQ ID NO 972; 510pp; English.  
XX CC The present invention relates to novel plant transcription factor  
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
CC sequences can be used to produce transgenic plants, which overexpress  
CC (II), where the transgenic plant has an altered trait as compared to a  
CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
CC an altered trait selected from increased tolerance to abiotic stress,  
CC increased tolerance to osmotic stress, increased tolerance to cold,  
CC increased germination in cold, increased tolerance to heat, increased  
CC germination in heat, increased tolerance to freezing conditions,  
CC increased tolerance to low nitrogen conditions, increased tolerance to  
CC low phosphate conditions, increased tolerance to disease, including  
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
CC increased tolerance to multiple fungal pathogens, increased resistance to

CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
CC flowering, altered flower structure, loss of flower determinacy, reduced  
CC fertility, altered shoot meristem development, altered branching pattern,  
CC altered stem morphology, altered vascular tissue structure, reduced  
CC apical dominance, altered trichome density, altered trichome development,  
CC altered trichome structure, altered root development, altered shade  
CC avoidance, altered seed development, altered seed ripening, altered seed  
CC germination, slow growth, fast growth, altered cell differentiation,  
CC altered cell proliferation, altered cell expansion, altered phase change,  
CC altered senescence, abnormal embryo development, altered programmed cell  
CC death, lethality when overexpressed, altered necrosis patterns, increased  
CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
CC green leaves, change in leaf shape, increased leaf size and mass, light  
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
CC altered seed coloration, altered seed size, altered seed shape, large  
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
CC content, altered seed protein content, altered seedprenyl content,  
CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
CC decreased anthocyanin levels. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 743 BP; 158 A; 210 C; 216 G; 159 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.73e-26 Length: 743  
Score: 248.00 Matches: 42  
Percent Similarity: 92.59% Conservative: 8  
Best Local Similarity: 77.78% Mismatches: 4  
Query Match: 83.22% Indels: 0  
DB: 12 Gaps: 0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADO62505 (1-743)

QY 1 AspGlyPheLysTrpArgLysTyrGlyLysSerValLysAsnAsnIleAsnLysArg 20  
DB 18 GACGGCTACAGTGGAGGAGTACGGCAAGAGTCCGTCAAGAACAGCCCCAACCAAG 77

QY 21 AsnTyrTyrLysCysSerSerGluGlyCysSerValLysValGluArgAspGly 40  
DB 78 AACTACTACCGTGTCTCGACGGAAGGGTCAACGTGAGAGCGGGTGGAGCGGACCAAG 137

QY 41 AspAspAlaAlaTyrValleThrThrTyrGluGlyValHis 54  
DB 138 GACGACCCAGCTACGTGTGACGAGTACGAGGGGATGCAC 179

RESULT 13  
ADO03196/c  
ID ADO03196 standard; cDNA; 974 BP.  
XX AC ADO03196;  
XX DT 01-JUL-2004 (first entry)  
XX DE Soybean orthologue of Thalecress transcription factor, cDNA #267.  
XX KW Soybean; transcription factor; ss; gene; plant; transgenic;  
KW abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;  
KW phosphate limitation; potassium limitation; nitrogen limitation;  
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
KW flowering; inflorescence architectural change;  
KW meristem cell differentiation; phyllotaxy; apical dominance;  
KW trichome development; seed development; premature senescence;  
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
KW seed morphology; secondary metabolism; light response; shade avoidance.  
XX OS Glycine max.  
XX PN US2004045049-A1.  
XX





CC defined in the specification or its complement. The method of the  
CC invention can be used to produced a plant having altered traits such as:  
CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone  
CC senitivity; disease resistance; sugar sensing; early or late flowering;  
CC altered flower structure, change in stem bifurcations, altered branching  
CC pattern, reduced apical dominance, reduced trichome density; lack of  
CC trichomes; reduced ectopic trichome development; altered trichome  
CC development; increase in trichome number; altered stem morphology;  
CC increased root growth; increased root hairs; altered seed development;  
CC altered cell proliferation or cell differentiation; rapid development;  
CC premature senescence; increased necrosis; increase in seedling or plant  
CC size; decreased plant size; leaf morphology; seed morphology; seed  
CC biochemistry; increase in root anthocyanins; increase in plant  
CC anthocyanins, or alteration in light response or shade avoidance. The  
CC transgenic plant, polynucleotides and polypeptides are useful in  
CC bioinformatic search methods. This sequence represents a plant  
CC transcription factor, and an orthologue of Arabidopsis thaliana  
CC transcription factors isolated in the invention, that can be used in the  
CC creation of a transgenic plant with altered traits.  
XX

SQ Sequence 1696 BP; 433 A; 436 C; 407 G; 420 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	2e-25	Length:	1696
Score:	244.00	Matches:	43
Percent Similarity:	88.89%	Conservative:	5
Best Local Similarity:	79.63%	Mismatches:	6
Query Match:	81.88%	Indels:	0
DB:	12	Gaps:	0

US-10-666-642-194\_COPY\_111\_164 (1-54) x ADI43067 (1-1696)

Qy	1	AspGlyPheLysTrpArgLysTyrGlyLysLysSerValLysAsnAsnIleAsnLysArg	20
Db	394	GATGATTCAATCGAGGAGTATGGCAAGAGGCTGTCAAGAGTAGCCCAATCCAAGG	453
Qy	21	AsnTyrTyrLysCysSerSerGluGlyCysSerValLysLysArgValGluArgAspGly	40
Db	454	AACTACTACCGCTGCTCGCGAGGGCTGCGCGGTGAAGAAGCGGTGGAGAGGACCGC	513
Qy	41	AspAspAlaAlaTyrValIleThrTyrGluGlyValHis	54
Db	514	GACGACCCCGCTACGTATCACCACCTACGACGCGCTCCAC	555

Search completed: August 26, 2005, 00:18:37  
Job time : 397 secs

**This Page Blank (uspto)**